

## SEQUENCE LISTING

<110> Verbsky, Michelle L.  
 Baublite, Catherine  
 Williams, Deryck J.  
 Kloek, Andrew P.  
 Davila-Aponte, Jennifer A.  
 Hresko, Michelle Coutu  
 McLaird, Merry B.

<120> NUCLEIC ACIDS ENCODING ANTHELMINTIC  
 AGENTS AND PLANTS MADE THEREFROM

<130> 12557-016001

<150> US 60/445,293  
 <151> 2003-02-05

<160> 130

<170> FastSEQ for Windows Version 4.0

<210> 1  
 <211> 1164  
 <212> DNA  
 <213> Ricinus communis

<220>  
 <221> CDS  
 <222> (1)...(1161)

<400> 1  
 atg gga ggt ggt ggt cgc atg tct act gtc ata acc agc aac aac agt 48  
 Met Gly Gly Gly Gly Arg Met Ser Thr Val Ile Thr Ser Asn Asn Ser  
 1 5 10 15  
 gag aag aaa gga gga agc agc cac ctt aag cga gcg ccg cac acg aag 96  
 Glu Lys Lys Gly Gly Ser Ser His Leu Lys Arg Ala Pro His Thr Lys  
 20 25 30  
 cct cct ttc aca ctt ggt gac ctc aag aga gcc atc cca ccc cat tgc 144  
 Pro Pro Phe Thr Leu Gly Asp Leu Lys Arg Ala Ile Pro Pro His Cys  
 35 40 45  
 ttt gaa cgc tct ttt gtg cgc tca ttc tcc tat gtt gcc tat gat gtc 192  
 Phe Glu Arg Ser Phe Val Arg Ser Phe Ser Tyr Val Ala Tyr Asp Val  
 50 55 60  
 tgc tta agt ttt ctt ttc tac tcg atc gcc acc aac ttc ttc cct tac 240  
 Cys Leu Ser Phe Leu Phe Tyr Ser Ile Ala Thr Asn Phe Phe Pro Tyr  
 65 70 75 80  
 atc tct tct ccg ctc tcg tat gtc gct tgg ctg gtt tac tgg ctc ttc 288  
 Ile Ser Ser Pro Leu Ser Tyr Val Ala Trp Leu Val Tyr Trp Leu Phe  
 85 90 95  
 caa ggc tgc att ctc act ggt ctt tgg gtc atc ggc cat gaa tgt ggc 336

Gln	Gly	Cys	Ile	Leu	Thr	Gly	Leu	Trp	Val	Ile	Gly	His	Glu	Cys	Gly		
			100					105					110				
cat	cat	gct	ttt	agt	gag	tat	cag	ctg	gct	gat	gac	att	gtt	ggc	cta		384
His	His	Ala	Phe	Ser	Glu	Tyr	Gln	Leu	Ala	Asp	Asp	Ile	Val	Gly	Leu		
		115					120					125					
att	gtc	cat	tct	gca	ctt	ctg	gtt	cca	tat	ttt	tca	tgg	aaa	tat	agc		432
Ile	Val	His	Ser	Ala	Leu	Leu	Val	Pro	Tyr	Phe	Ser	Trp	Lys	Tyr	Ser		
	130					135					140						
cat	cgc	cgc	cac	cat	tct	aac	ata	gga	tct	ctc	gag	cga	gac	gaa	gtg		480
His	Arg	Arg	His	His	Ser	Asn	Ile	Gly	Ser	Leu	Glu	Arg	Asp	Glu	Val		
145					150					155					160		
ttc	gtc	ccg	aaa	tca	aag	tcg	aaa	att	tca	tgg	tat	tct	aag	tac	tta		528
Phe	Val	Pro	Lys	Ser	Lys	Ser	Lys	Ile	Ser	Trp	Tyr	Ser	Lys	Tyr	Leu		
				165				170						175			
aac	aac	ccg	cca	ggt	cga	gtt	ttg	aca	ctt	gct	gcc	acg	ctc	ctc	ctt		576
Asn	Asn	Pro	Pro	Gly	Arg	Val	Leu	Thr	Leu	Ala	Ala	Thr	Leu	Leu	Leu		
			180				185						190				
ggc	tgg	cct	tta	tac	tta	gct	ttc	aat	gtc	tct	ggt	aga	cct	tac	gat		624
Gly	Trp	Pro	Leu	Tyr	Leu	Ala	Phe	Asn	Val	Ser	Gly	Arg	Pro	Tyr	Asp		
		195				200						205					
cgc	ttt	gct	tgc	cat	tat	gat	ccc	tat	ggc	cca	ata	ttt	tcc	gaa	aga		672
Arg	Phe	Ala	Cys	His	Tyr	Asp	Pro	Tyr	Gly	Pro	Ile	Phe	Ser	Glu	Arg		
	210					215				220							
gaa	agg	ctt	cag	att	tac	att	gct	gac	ctc	gga	atc	ttt	gcc	aca	acg		720
Glu	Arg	Leu	Gln	Ile	Tyr	Ile	Ala	Asp	Leu	Gly	Ile	Phe	Ala	Thr	Thr		
225				230					235						240		
ttt	gtg	ctt	tat	cag	gct	aca	atg	gca	aaa	ggg	ttg	gct	tgg	gta	atg		768
Phe	Val	Leu	Tyr	Gln	Ala	Thr	Met	Ala	Lys	Gly	Leu	Ala	Trp	Val	Met		
				245				250						255			
cgT	atc	tat	ggg	gtg	cca	ttg	ctt	att	gtt	aac	tgt	ttc	ctt	gtt	atg		816
Arg	Ile	Tyr	Gly	Val	Pro	Leu	Leu	Ile	Val	Asn	Cys	Phe	Leu	Val	Met		
			260					265					270				
atc	aca	tac	ttg	cag	cac	act	cac	cca	gct	att	cca	cgc	tat	ggc	tca		864
Ile	Thr	Tyr	Leu	Gln	His	Thr	His	Pro	Ala	Ile	Pro	Arg	Tyr	Gly	Ser		
			275				280					285					
tcg	gaa	tgg	gat	tgg	ctc	cgg	gga	gca	atg	gtg	act	gtc	gat	aga	gat		912
Ser	Glu	Trp	Asp	Trp	Leu	Arg	Gly	Ala	Met	Val	Thr	Val	Asp	Arg	Asp		
	290					295					300						
tat	ggg	gtg	ttg	aat	aaa	gta	ttc	cat	aac	att	gca	gac	act	cat	gta		960
Tyr	Gly	Val	Leu	Asn	Lys	Val	Phe	His	Asn	Ile	Ala	Asp	Thr	His	Val		
305				310						315					320		
gct	cat	cat	ctc	ttt	gct	aca	gtg	cca	cat	tac	cat	gca	atg	gag	gcc		1008
Ala	His	His	Leu	Phe	Ala	Thr	Val	Pro	His	Tyr	His	Ala	Met	Glu	Ala		

	325	330	335	
act aaa gca atc aag cct ata atg ggt gag tat tac cgg tat gat ggt				1056
Thr Lys Ala Ile Lys Pro Ile Met Gly Glu Tyr Tyr Arg Tyr Asp Gly	340	345	350	
acc cca ttt tac aag gca ttg tgg agg gag gca aag gag tgc ttg ttc				1104
Thr Pro Phe Tyr Lys Ala Leu Trp Arg Glu Ala Lys Glu Cys Leu Phe	355	360	365	
gtc gag cca gat gaa gga gct cct aca caa ggc gtt ttc tgg tac cgg				1152
Val Glu Pro Asp Glu Gly Ala Pro Thr Gln Gly Val Phe Trp Tyr Arg	370	375	380	
aac aag tat taa				1164
Asn Lys Tyr				
385				
<210> 2				
<211> 1155				
<212> DNA				
<213> <i>Lesquerella fendleri</i>				
<220>				
<221> CDS				
<222> (1) ... (1152)				
<400> 2				
atg ggt gct ggt gga aga ata atg gtt acc ccc tct tcc aag aaa tca				48
Met Gly Ala Gly Gly Arg Ile Met Val Thr Pro Ser Ser Lys Lys Ser	1	5	10	15
gaa act gaa gcc cta aaa cgt gga cca tgt gag aaa cca cca ttc act				96
Glu Thr Glu Ala Leu Lys Arg Gly Pro Cys Glu Lys Pro Pro Phe Thr	20	25	30	
gtt aaa gat ctg aag aaa gca atc cca cag cat tgt ttt cag cgc tct				144
Val Lys Asp Leu Lys Lys Ala Ile Pro Gln His Cys Phe Gln Arg Ser	35	40	45	
atc cct cgt tct ttc tcc tac ctt ctc aca gat atc act tta gtt tct				192
Ile Pro Arg Ser Phe Ser Tyr Leu Leu Thr Asp Ile Thr Leu Val Ser	50	55	60	
tgc ttc tac tac gtt gcc aca aat tac ttc tct ctt ctt cct cag cct				240
Cys Phe Tyr Tyr Val Ala Thr Asn Tyr Phe Ser Leu Leu Pro Gln Pro	65	70	75	80
ctc tct act tac cta gct tgg cct ctc tat tgg gta tgt caa ggc tgt				288
Leu Ser Thr Tyr Leu Ala Trp Pro Leu Tyr Trp Val Cys Gln Gly Cys	85	90	95	
gtc tta aca ggt atc tgg gtc att ggc cat gaa tgt ggt cac cat gca				336
Val Leu Thr Gly Ile Trp Val Ile Gly His Glu Cys Gly His His Ala	100	105	110	
ttc agt gac tat caa tgg gta gat gac act gtt ggt ttt atc ttc cat				384

Phe	Ser	Asp	Tyr	Gln	Trp	Val	Asp	Asp	Thr	Val	Gly	Phe	Ile	Phe	His		
		115					120					125					
tcc	ttc	ctt	ctc	gtc	cct	tac	ttc	tcc	tgg	aaa	tac	agt	cat	cgt	cgt		432
Ser	Phe	Leu	Leu	Val	Pro	Tyr	Phe	Ser	Trp	Lys	Tyr	Ser	His	Arg	Arg		
	130					135				140							
cac	cat	tcc	aac	aat	gga	tct	ctc	gag	aaa	gat	gaa	gtc	ttt	gtc	cca		480
His	His	Ser	Asn	Asn	Gly	Ser	Leu	Glu	Lys	Asp	Glu	Val	Phe	Val	Pro		
	145				150					155					160		
ccg	aaa	aaa	gct	gca	gtc	aaa	tgg	tat	gtt	aaa	tac	ctc	aac	aac	cct		528
Pro	Lys	Lys	Ala	Ala	Val	Lys	Trp	Tyr	Val	Lys	Tyr	Leu	Asn	Asn	Pro		
				165				170						175			
ctt	gga	cgc	att	ctg	gtg	tta	aca	gtt	cag	ttt	atc	ctc	ggg	tgg	cct		576
Leu	Gly	Arg	Ile	Leu	Val	Leu	Thr	Val	Gln	Phe	Ile	Leu	Gly	Trp	Pro		
			180					185					190				
ttg	tat	cta	ccc	ttt	aat	gta	tca	ggt	aga	cct	tat	gat	ggt	ttc	gct		624
Leu	Tyr	Leu	Pro	Phe	Asn	Val	Ser	Gly	Arg	Pro	Tyr	Asp	Gly	Phe	Ala		
		195					200					205					
tca	cat	ttc	ttc	cct	cat	gca	cct	atc	ttt	aaa	gac	cgc	gaa	cgt	ctc		672
Ser	His	Phe	Phe	Pro	His	Ala	Pro	Ile	Phe	Lys	Asp	Arg	Glu	Arg	Leu		
		210				215					220						
cag	ata	tac	atc	tca	gat	gct	ggt	att	cta	gct	gtc	tgt	tat	ggt	ctt		720
Gln	Ile	Tyr	Ile	Ser	Asp	Ala	Gly	Ile	Leu	Ala	Val	Cys	Tyr	Gly	Leu		
	225				230					235					240		
tac	cgt	tac	gct	gct	tca	caa	gga	ttg	act	gct	atg	atc	tgc	gtc	tat		768
Tyr	Arg	Tyr	Ala	Ala	Ser	Gln	Gly	Leu	Thr	Ala	Met	Ile	Cys	Val	Tyr		
				245					250					255			
gga	gta	ccg	ctt	ttg	ata	gtg	aac	ttt	ttc	ctt	gtc	ttg	gta	act	ttc		816
Gly	Val	Pro	Leu	Leu	Ile	Val	Asn	Phe	Phe	Leu	Val	Leu	Val	Thr	Phe		
			260					265					270				
ttg	cag	cac	act	cat	cct	tcg	tta	cct	cac	tat	gat	tca	acc	gag	tgg		864
Leu	Gln	His	Thr	His	Pro	Ser	Leu	Pro	His	Tyr	Asp	Ser	Thr	Glu	Trp		
		275					280					285					
gaa	tgg	att	aga	gga	gct	ttg	gtt	acg	gta	gac	aga	gac	tat	gga	atc		912
Glu	Trp	Ile	Arg	Gly	Ala	Leu	Val	Thr	Val	Asp	Arg	Asp	Tyr	Gly	Ile		
		290				295				300							
ttg	aac	aag	gtg	ttt	cac	aac	ata	aca	gac	aca	cat	gtg	gct	cat	cat		960
Leu	Asn	Lys	Val	Phe	His	Asn	Ile	Thr	Asp	Thr	His	Val	Ala	His	His		
	305				310					315					320		
ctc	ttt	gca	act	ata	ccg	cat	tat	aac	gca	atg	gaa	gct	aca	gag	gcg		1008
Leu	Phe	Ala	Thr	Ile	Pro	His	Tyr	Asn	Ala	Met	Glu	Ala	Thr	Glu	Ala		
				325					330					335			
ata	aag	cca	ata	ctt	ggt	gat	tac	tac	cac	ttc	gat	gga	aca	ccg	tgg		1056
Ile	Lys	Pro	Ile	Leu	Gly	Asp	Tyr	Tyr	His	Phe	Asp	Gly	Thr	Pro	Trp		

	340		345		350											
tat	gtg	gcc	atg	tat	agg	gaa	gca	aag	gag	tgt	ctc	tat	gta	gaa	ccg	1104
Tyr	Val	Ala	Met	Tyr	Arg	Glu	Ala	Lys	Glu	Cys	Leu	Tyr	Val	Glu	Pro	
		355					360						365			
gat	acg	gaa	cgt	ggg	aag	aaa	ggg	gtg	tac	tat	tac	aac	aat	aag	tta	1152
Asp	Thr	Glu	Arg	Gly	Lys	Lys	Gly	Val	Tyr	Tyr	Tyr	Asn	Asn	Lys	Leu	
	370					375					380					
tga																1155
<210>	3															
<211>	1152															
<212>	DNA															
<213>	Lesquerella	lindheimeri														
<220>																
<221>	CDS															
<222>	(1)...	(1149)														
<400>	3															
atg	ggt	gct	ggt	gga	aga	ata	atg	ggt	acc	ccc	tct	tcc	aag	aaa	tcg	48
Met	Gly	Ala	Gly	Gly	Arg	Ile	Met	Val	Thr	Pro	Ser	Ser	Lys	Lys	Ser	
	1			5				10						15		
aaa	cct	gaa	gcc	cta	aga	cgt	ggg	cca	ggt	gag	aaa	cca	cca	ttc	act	96
Lys	Pro	Glu	Ala	Leu	Arg	Arg	Gly	Pro	Gly	Glu	Lys	Pro	Pro	Phe	Thr	
			20				25						30			
ggt	caa	gat	cta	agg	aaa	gca	atc	cca	cgg	cat	tgt	ttc	aaa	cgc	tct	144
Val	Gln	Asp	Leu	Arg	Lys	Ala	Ile	Pro	Arg	His	Cys	Phe	Lys	Arg	Ser	
		35				40						45				
atc	cct	cgt	tct	ttc	tcc	tat	ctt	ctc	aca	gat	atc	att	tta	gct	tct	192
Ile	Pro	Arg	Ser	Phe	Ser	Tyr	Leu	Leu	Thr	Asp	Ile	Ile	Leu	Ala	Ser	
	50					55				60						
tgc	ttc	tac	tac	gtg	gcc	acc	aat	tac	ttc	tca	ctt	ctt	cca	cag	cct	240
Cys	Phe	Tyr	Tyr	Val	Ala	Thr	Asn	Tyr	Phe	Ser	Leu	Leu	Pro	Gln	Pro	
	65			70				75						80		
ctc	tct	act	tac	ttt	gct	tgg	cct	ctc	tat	tgg	gta	tgt	caa	ggc	tgt	288
Leu	Ser	Thr	Tyr	Phe	Ala	Trp	Pro	Leu	Tyr	Trp	Val	Cys	Gln	Gly	Cys	
				85			90							95		
gtc	tta	acc	ggt	ggt	tgg	gtc	ctt	ggc	cat	gaa	tgt	ggt	cac	caa	gca	336
Val	Leu	Thr	Gly	Val	Trp	Val	Leu	Gly	His	Glu	Cys	Gly	His	Gln	Ala	
			100				105						110			
ttt	agt	gac	tat	caa	tgg	gta	gat	gac	act	ggt	ggt	ttt	atc	atc	cat	384
Phe	Ser	Asp	Tyr	Gln	Trp	Val	Asp	Asp	Thr	Val	Gly	Phe	Ile	Ile	His	
		115					120					125				
acc	ttc	ctc	ctc	atc	cct	tac	ttc	tcc	tgg	aag	tat	agt	cat	cgt	cgt	432
Thr	Phe	Leu	Leu	Ile	Pro	Tyr	Phe	Ser	Trp	Lys	Tyr	Ser	His	Arg	Arg	
	130					135					140					

cac cat gcc aat aat gga tca ctc gag aga gat gaa gtc ttt gtc cca	480
His His Ala Asn Asn Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro	
145 150 155 160	
ccg aag aaa gct gca gtc aaa tgg tat gtc aaa tac ctc aac aac cct	528
Pro Lys Lys Ala Ala Val Lys Trp Tyr Val Lys Tyr Leu Asn Asn Pro	
165 170 175	
ctt gga cgc act gtg gtg tta ata gtc cag ttt gtc ctc gga tgg ccc	576
Leu Gly Arg Thr Val Val Leu Ile Val Gln Phe Val Leu Gly Trp Pro	
180 185 190	
ttg tac cta gcc ttt aac gta tca ggt aga tcc tat gat ggt ttc gct	624
Leu Tyr Leu Ala Phe Asn Val Ser Gly Arg Ser Tyr Asp Gly Phe Ala	
195 200 205	
tca cat ttc ttc cca cat gca ccc atc ttc aag gac cga gaa cgt ctc	672
Ser His Phe Phe Pro His Ala Pro Ile Phe Lys Asp Arg Glu Arg Leu	
210 215 220	
cat ata tac atc aca gat gct ggt att cta gct gtc tgt tat ggt ctt	720
His Ile Tyr Ile Thr Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu	
225 230 235 240	
tac cgt tac gca gct aca aaa gga ttg acc gct atg atc tgc gtc tat	768
Tyr Arg Tyr Ala Ala Thr Lys Gly Leu Thr Ala Met Ile Cys Val Tyr	
245 250 255	
ggg gta cct cct ctg gtt gta aac ttt ttc ctt gtc ttg gtc act ttc	816
Gly Val Pro Leu Val Val Asn Phe Phe Leu Val Leu Val Thr Phe	
260 265 270	
ttg cag cac act cat cct tca tta cct cac tat gat tca acc gag tgg	864
Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Thr Glu Trp	
275 280 285	
gac tgg att aga gga gcc atg gtt aca gta gac aga gac tat ggg atc	912
Asp Trp Ile Arg Gly Ala Met Val Thr Val Asp Arg Asp Tyr Gly Ile	
290 295 300	
ttg aac aag gtg ttc cac aac ata aca gac aca cat gtg gct cat cat	960
Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His	
305 310 315 320	
ctt ttc gca aca ata ccg cat tat aat gca atg gaa gct aca gag gcg	1008
Leu Phe Ala Thr Ile Pro His Tyr Asn Ala Met Glu Ala Thr Glu Ala	
325 330 335	
ata aag cca ata ctc gga gac tac tac cat ttc gat gga aca ccc tgg	1056
Ile Lys Pro Ile Leu Gly Asp Tyr Tyr His Phe Asp Gly Thr Pro Trp	
340 345 350	
tat gtg gct atg tat agg gaa gca aag cag tgt ctc tat gta gaa cag	1104
Tyr Val Ala Met Tyr Arg Glu Ala Lys Gln Cys Leu Tyr Val Glu Gln	
355 360 365	

gat aca gaa aag aag aaa ggt gtc tac tat tac aac aat aag tta 1149  
Asp Thr Glu Lys Lys Lys Gly Val Tyr Tyr Tyr Asn Asn Lys Leu  
370 375 380

tga 1152

<210> 4  
<211> 1155  
<212> DNA  
<213> *Lesquerella gracilis* A

<220>  
<221> CDS  
<222> (1)...(1152)

<400> 4

atg ggt gct ggt gga aga ata atg gta acc ccc tct tcg aag aaa tcg 48  
Met Gly Ala Gly Gly Arg Ile Met Val Thr Pro Ser Ser Lys Lys Ser  
1 5 10 15

aaa cct caa gcc cta aga cgt gga cca tgt gag aaa cca cca ttc act 96  
Lys Pro Gln Ala Leu Arg Arg Gly Pro Cys Glu Lys Pro Pro Phe Thr  
20 25 30

gtt aaa gat ctg aag aaa gca atc cca ccg cat tgt ttc aaa cgc tct 144  
Val Lys Asp Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser  
35 40 45

atc cct cgc tct ttc tct tac ctt ctc aca gat ttc att cta gct tct 192  
Ile Pro Arg Ser Phe Ser Tyr Leu Leu Thr Asp Phe Ile Leu Ala Ser  
50 55 60

tgc ttc tac tac gtg gct aca aat tac ttc tct ctt ctc cca cag cct 240  
Cys Phe Tyr Tyr Val Ala Thr Asn Tyr Phe Ser Leu Leu Pro Gln Pro  
65 70 75 80

gtc tct aat tac ctg gct tgg cct ctc tat tgg ata tgt caa ggc tgt 288  
Val Ser Asn Tyr Leu Ala Trp Pro Leu Tyr Trp Ile Cys Gln Gly Cys  
85 90 95

gtc tta acc ggt gtt tgg gtc ctt ggc cat gaa tgt ggt cac cat gca 336  
Val Leu Thr Gly Val Trp Val Leu Gly His Glu Cys Gly His His Ala  
100 105 110

ttc agt gac tat caa tgg gta gat gac act gtt ggt ttt atc atc cat 384  
Phe Ser Asp Tyr Gln Trp Val Asp Asp Thr Val Gly Phe Ile Ile His  
115 120 125

tcc ttc ctc ctt gtc cct tac ttc tcc tgg aag tac agt cat cgt cgt 432  
Ser Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg  
130 135 140

cac cat tcc aac aat gga tcc ctc gag aaa gat gaa gtc ttt gtt cca 480  
His His Ser Asn Asn Gly Ser Leu Glu Lys Asp Glu Val Phe Val Pro  
145 150 155 160

cct aag aaa gct gca gtc aaa tgg tat gtt aag tac ctc aac aac cct 528

Pro Lys Lys Ala Ala Val Lys Trp Tyr Val Lys Tyr Leu Asn Asn Pro	
165	170 175
ctt gga cgc act gtg gtg tta ata gtc cag ttt gtc ctc ggg tgg cct	576
Leu Gly Arg Thr Val Val Leu Ile Val Gln Phe Val Leu Gly Trp Pro	
180	185 190
ttg tat cta gcc ttt aac gta tca ggt aga ccc tat gat ggg ttc gct	624
Leu Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Phe Ala	
195	200 205
tca cac ttc ttt cct cat gca ccc atc ttc agg gac cgt gaa cgc ctc	672
Ser His Phe Phe Pro His Ala Pro Ile Phe Arg Asp Arg Glu Arg Leu	
210	215 220
cat ata tac atc aca gat gct ggt att cta gct gtc tgt tat ggt ctt	720
His Ile Tyr Ile Thr Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu	
225	230 235 240
tac cgt tac gct gct tca aaa gga ttg acc gct atg atc tgc gtc tac	768
Tyr Arg Tyr Ala Ala Ser Lys Gly Leu Thr Ala Met Ile Cys Val Tyr	
245	250 255
gga gta ccg ctt ttg ata gtg aac ttt ttc ctc gtg ttg gtc act ttc	816
Gly Val Pro Leu Leu Ile Val Asn Phe Phe Leu Val Leu Val Thr Phe	
260	265 270
ttg cag cac act cat cct tca tta cct cac tat gat tca acc gag tgg	864
Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Thr Glu Trp	
275	280 285
gaa tgg att aga gga gcc ttg gtt aca gta gac aga gac tat gga atc	912
Glu Trp Ile Arg Gly Ala Leu Val Thr Val Asp Arg Asp Tyr Gly Ile	
290	295 300
ttg aac aag gtg ttc cac aac ata aca gac aca cat gtg gct cat cat	960
Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His	
305	310 315 320
att ttc gca aca ata ccg cat tat aat gca atg gaa gct aca gag gcg	1008
Ile Phe Ala Thr Ile Pro His Tyr Asn Ala Met Glu Ala Thr Glu Ala	
325	330 335
ata aag cca ata ctc gga gac tac tac cat ttc gat gga aca ccg tgg	1056
Ile Lys Pro Ile Leu Gly Asp Tyr Tyr His Phe Asp Gly Thr Pro Trp	
340	345 350
tat gtg gcc atg tac agg gaa gca aag gag tgt ctc tat gta gaa cag	1104
Tyr Val Ala Met Tyr Arg Glu Ala Lys Glu Cys Leu Tyr Val Glu Gln	
355	360 365
gat aca gaa cgt ggg aag aaa ggt gtc tac tat tac aac aat aag tta	1152
Asp Thr Glu Arg Gly Lys Lys Gly Val Tyr Tyr Tyr Asn Asn Lys Leu	
370	375 380
tga	1155



<210> 5  
 <211> 1155  
 <212> DNA  
 <213> *Lesquerella gracilis* B

<220>  
 <221> CDS  
 <222> (1) ... (1152)

<400> 5  
 atg ggt gct ggt gga aga ata atg gtt acc cct tct tcc aag aaa tca 48  
 Met Gly Ala Gly Gly Arg Ile Met Val Thr Pro Ser Ser Lys Lys Ser  
 1 5 10 15

gaa act gaa gcc cta aaa cgt gga cca tgt gag aaa cca cca ttc act 96  
 Glu Thr Glu Ala Leu Lys Arg Gly Pro Cys Glu Lys Pro Pro Phe Thr  
 20 25 30

gtt aaa gat ctg aag aaa gca atc cca cag cat tgt ttt caa cgc tct 144  
 Val Lys Asp Leu Lys Lys Ala Ile Pro Gln His Cys Phe Gln Arg Ser  
 35 40 45

atc cct cgt tct ttc tcc tac ctt ctc aca gat atc act tta gtt tct 192  
 Ile Pro Arg Ser Phe Ser Tyr Leu Leu Thr Asp Ile Thr Leu Val Ser  
 50 55 60

tgc ttc tac tac gtt gcc aca aat tac ttc tct ctt ctt cct cag cct 240  
 Cys Phe Tyr Tyr Val Ala Thr Asn Tyr Phe Ser Leu Leu Pro Gln Pro  
 65 70 75 80

ctc tct act tac cta gct tgg cct ctc tat tgg gta tgt caa ggc tgt 288  
 Leu Ser Thr Tyr Leu Ala Trp Pro Leu Tyr Trp Val Cys Gln Gly Cys  
 85 90 95

gtc cta aca ggt atc tgg gtc ctt ggc cat gaa tgt ggt cac cat gca 336  
 Val Leu Thr Gly Ile Trp Val Leu Gly His Glu Cys Gly His His Ala  
 100 105 110

ttc agt gac tat caa tgg cta gat gac act gtt ggt ttt atc ttc cat 384  
 Phe Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Phe Ile Phe His  
 115 120 125

tcc tta ctt ctc gtc cct tac ttc tcc tgg aaa tac agt cat cgt cgt 432  
 Ser Leu Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg  
 130 135 140

cac cat tcc aac aat gga tct ctc gag aaa gat gaa gtc ttt gtc cca 480  
 His His Ser Asn Asn Gly Ser Leu Glu Lys Asp Glu Val Phe Val Pro  
 145 150 155 160

ccg aaa aaa gct gca gtc aaa tgg tat gtt aaa tac ctc aac aac cct 528  
 Pro Lys Lys Ala Ala Val Lys Trp Tyr Val Lys Tyr Leu Asn Asn Pro  
 165 170 175

ctt gga cgc att ctg gtg tta aca gtt cgg ttt atc ctc ggg tgg cct 576  
 Leu Gly Arg Ile Leu Val Leu Thr Val Arg Phe Ile Leu Gly Trp Pro  
 180 185 190

ttg tat cta gcc ttt aat gta tca ggt aga cct tat gat ggt ttc gct Leu Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Phe Ala 195 200 205	624
tca cat ttc ttc cct cat gca cct atc ttt aaa gac cgc gaa cgt ctc Ser His Phe Phe Pro His Ala Pro Ile Phe Lys Asp Arg Glu Arg Leu 210 215 220	672
cag ata tac atc tca gat gct ggt att cta gct gtc tgt tat ggt ctt Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Thr Ala Val Cys Tyr Gly Leu 225 230 235 240	720
tac cgt tac gct gct tca caa gga ttg acc gct atg atc tgc gtc tat Tyr Arg Tyr Ala Ala Ser Gln Gly Leu Thr Ala Met Ile Cys Val Tyr 245 250 255	768
gga gta ccg ctt ttg ata gtg aac ttt ttc ctt gtc ttg gta act ttc Gly Val Pro Leu Leu Ile Val Asn Phe Phe Leu Val Leu Val Thr Phe 260 265 270	816
ttg cag cac act cat cct tcg tta cct cac tat gat tca acc gag tgg Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Thr Glu Trp 275 280 285	864
gaa tgg att aga gga gct ttg gtt acg gta gac aga gac tac gga atc Glu Trp Ile Arg Gly Ala Leu Val Thr Val Asp Arg Asp Tyr Gly Ile 290 295 300	912
ttg aac aag gtg ttt cac aac ata aca gac aca cat gtg gct cat cat Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His 305 310 315 320	960
ctt ttc gca act ata ccg cat tat aac gca atg gaa gct aca gag gcg Leu Phe Ala Thr Ile Pro His Tyr Asn Ala Met Glu Ala Thr Glu Ala 325 330 335	1008
ata aag cca ata ctt ggt gat tac tac cat ttc gat gga aca ccg tgg Ile Lys Pro Ile Leu Gly Asp Tyr Tyr His Phe Asp Gly Thr Pro Trp 340 345 350	1056
tat gtg gct atg tat agg gaa gca aag gag tgt ctc tat gta gaa ccg Tyr Val Ala Met Tyr Arg Glu Ala Lys Glu Cys Leu Tyr Val Glu Pro 355 360 365	1104
gat acg gaa cgt ggg aag aaa ggt gtc tac tat tac aac aat aag tta Asp Thr Glu Arg Gly Lys Lys Gly Val Tyr Tyr Tyr Asn Asn Lys Leu 370 375 380	1152
tga	1155

&lt;210&gt; 6

&lt;211&gt; 1125

&lt;212&gt; DNA

&lt;213&gt; Crepis biennis

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(1122)

&lt;400&gt; 6

atg ggt gcc cac ggc cat ggt cga aca tcg aaa aaa tcg gtc atg gaa	48
Met Gly Ala His Gly His Gly Arg Thr Ser Lys Lys Ser Val Met Glu	
1 5 10 15	
cgt gtc tcg gtt gat cca gta ccc ttc tcg cta agt gat tta aag caa	96
Arg Val Ser Val Asp Pro Val Pro Phe Ser Leu Ser Asp Leu Lys Gln	
20 25 30	
gca atc cct ccc cat tgc ttc cag cga tct gtc atc cgt tca tct tac	144
Ala Ile Pro Pro His Cys Phe Gln Arg Ser Val Ile Arg Ser Ser Tyr	
35 40 45	
tat gta gtt cac gat ctc att att gcc tac atc ttc tac ttc ctt gcc	192
Tyr Val Val His Asp Leu Ile Ile Ala Tyr Ile Phe Tyr Phe Leu Ala	
50 55 60	
gat aaa tat att ccg att ctc cct gct cct cta gcc tac tta gct tgg	240
Asp Lys Tyr Ile Pro Ile Leu Pro Ala Pro Leu Ala Tyr Leu Ala Trp	
65 70 75 80	
ccc ctt tac tgg ttc tgt caa gct agc atc ctc act ggt tta tgg atc	288
Pro Leu Tyr Trp Phe Cys Gln Ala Ser Ile Leu Thr Gly Leu Trp Ile	
85 90 95	
ctc ggt cat gaa tgc ggt cac cat gcc ttt agc gag tac caa tgg gtt	336
Leu Gly His Glu Cys Gly His His Ala Phe Ser Glu Tyr Gln Trp Val	
100 105 110	
gac gac act gtg ggc ttc atg gtc cac tca ttt ctc ctc acc ccg tat	384
Asp Asp Thr Val Gly Phe Met Val His Ser Phe Leu Leu Thr Pro Tyr	
115 120 125	
ttc tcg tgg aaa tac agt cac cgg aat cac cat gcc aac aca agt tcc	432
Phe Ser Trp Lys Tyr Ser His Arg Asn His His Ala Asn Thr Ser Ser	
130 135 140	
atc gat aac gat gaa gtt tac att ccg aaa agc aag tcc aaa ctc gcg	480
Ile Asp Asn Asp Glu Val Tyr Ile Pro Lys Ser Lys Ser Lys Leu Ala	
145 150 155 160	
ctt acc tat aaa ctt ctt aac aac ccg cct ggt cga ctg tta gtt atg	528
Leu Thr Tyr Lys Leu Leu Asn Asn Pro Pro Gly Arg Leu Leu Val Met	
165 170 175	
gtt atc atg ttc acc cta gga ttt cct tta tac ctc ttg aca aat att	576
Val Ile Met Phe Thr Leu Gly Phe Pro Leu Tyr Leu Leu Thr Asn Ile	
180 185 190	
tcc ggc aag aag tac gac agg ttt gcc aac cac ttc gac ccc atg agt	624
Ser Gly Lys Lys Tyr Asp Arg Phe Ala Asn His Phe Asp Pro Met Ser	
195 200 205	
cca att ttc aag gaa cgt gag cgg ttt cag gtc ttg ctt tcg gat ctt	672

Pro	Ile	Phe	Lys	Glu	Arg	Glu	Arg	Phe	Gln	Val	Leu	Leu	Ser	Asp	Leu		
	210					215					220						
ggc	ctt	ctt	gct	gtg	ttt	tat	gga	att	aaa	gtt	gct	gta	gca	aag	aaa		720
Gly	Leu	Leu	Ala	Val	Phe	Tyr	Gly	Ile	Lys	Val	Ala	Val	Ala	Lys	Lys		
225					230				235						240		
gga	gct	gcg	tgg	gtg	gcg	tgt	atg	tat	gga	gtt	ccg	atg	cta	ggc	gta		768
Gly	Ala	Ala	Trp	Val	Ala	Cys	Met	Tyr	Gly	Val	Pro	Met	Leu	Gly	Val		
				245					250					255			
ttt	acc	ctt	ttc	gat	atc	atc	acg	tac	ttg	cac	cac	acc	cat	cag	tcg		816
Phe	Thr	Leu	Phe	Asp	Ile	Ile	Thr	Tyr	Leu	His	His	Thr	His	Gln	Ser		
			260					265					270				
tct	cct	cat	tat	gac	tca	act	gaa	tgg	aac	tgg	atc	aga	ggg	gcg	ttg		864
Ser	Pro	His	Tyr	Asp	Ser	Thr	Glu	Trp	Asn	Trp	Ile	Arg	Gly	Ala	Leu		
		275					280					285					
tca	gca	atc	gat	agg	gac	ttt	ggg	ttc	atg	aat	agt	gtt	ttc	cat	gat		912
Ser	Ala	Ile	Asp	Arg	Asp	Phe	Gly	Phe	Met	Asn	Ser	Val	Phe	His	Asp		
	290					295			300								
gtt	aca	cac	act	cac	gtc	atg	cat	cat	atg	ttt	tca	tac	att	cca	cac		960
Val	Thr	His	Thr	His	Val	Met	His	His	Met	Phe	Ser	Tyr	Ile	Pro	His		
305					310				315						320		
tat	cat	gcg	aaa	gag	gca	agg	gat	gca	atc	aat	aca	atc	ata	ggc	gac		1008
Tyr	His	Ala	Lys	Glu	Ala	Arg	Asp	Ala	Ile	Asn	Thr	Ile	Ile	Gly	Asp		
				325				330						335			
tat	tat	atg	atc	gat	agg	act	cca	att	ttg	aaa	gca	ctg	tgg	aga	gag		1056
Tyr	Tyr	Met	Ile	Asp	Arg	Thr	Pro	Ile	Leu	Lys	Ala	Leu	Trp	Arg	Glu		
			340					345					350				
gcc	aag	gaa	tgc	atg	tac	atc	gag	cct	gat	agc	aag	cgc	aaa	ggg	gta		1104
Ala	Lys	Glu	Cys	Met	Tyr	Ile	Glu	Pro	Asp	Ser	Lys	Arg	Lys	Gly	Val		
		355					360				365						
tat	tgg	tac	cat	aaa	ttg	tga											1125
Tyr	Trp	Tyr	His	Lys	Leu												
	370																
<210>	7																
<211>	1152																
<212>	DNA																
<213>	Ricinus communis																
<220>																	
<221>	CDS																
<222>	(1)...(1149)																
<400>	7																
atg	ggg	gca	ggg	gga	aga	atg	ccg	ggt	cct	act	tct	tcc	aag	aaa	tcg		48
Met	Gly	Ala	Gly	Gly	Arg	Met	Pro	Val	Pro	Thr	Ser	Ser	Lys	Lys	Ser		
1				5					10					15			

gaa acc gac acc aca aag cgt gtg ccg tgc gag aaa ccg cct ttc tcg Glu Thr Asp Thr Thr Lys Arg Val Pro Cys Glu Lys Pro Pro Phe Ser 20 25 30	96
gtg gga gat ctg aag aaa gcc atc cca ccc cat tgc ttt gaa cgc tct Val Gly Asp Leu Lys Lys Ala Ile Pro Pro His Cys Phe Glu Arg Ser 35 40 45	144
ttt gtg cgc tca ttc tcc tat gtt gcc tat gat gtc tgc tta agt ttt Phe Val Arg Ser Phe Ser Tyr Val Ala Tyr Asp Val Cys Leu Ser Phe 50 55 60	192
ctt ttc tac tcg atc gcc acc aac ttc ttc cct tac atc tct tct ccg Leu Phe Tyr Ser Ile Ala Thr Asn Phe Phe Pro Tyr Ile Ser Ser Pro 65 70 75 80	240
ctc tcg tat gtc gct tgg ctg gtt tac tgg ctc ttc caa ggc tgc att Leu Ser Tyr Val Ala Trp Leu Val Tyr Trp Leu Phe Gln Gly Cys Ile 85 90 95	288
ctc act ggt ctt tgg gtc atc ggc cat gaa tgt ggc cat cat gct ttt Leu Thr Gly Leu Trp Val Ile Gly His Glu Cys Gly His His Ala Phe 100 105 110	336
agt gag tat cag ctg gct gat gac att gtt ggc cta att gtc cat tct Ser Glu Tyr Gln Leu Ala Asp Asp Ile Val Gly Leu Ile Val His Ser 115 120 125	384
gca ctt ctg gtt cca tat ttt tca tgg aaa tat agc cat cgc cgc cac Ala Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg His 130 135 140	432
cat tct aac ata gga tct ctc gag cga gac gaa gtg ttc gtc ccg aaa His Ser Asn Ile Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys 145 150 155 160	480
tca aag tcg aaa att tca tgg tat tct aag tac tta aac aac ccg cca Ser Lys Ser Lys Ile Ser Trp Tyr Ser Lys Tyr Leu Asn Asn Pro Pro 165 170 175	528
ggt cga gtt ttg aca ctt gct gcc acg ctc ctc ctt ggc tgg cct tta Gly Arg Val Leu Thr Leu Ala Ala Thr Leu Leu Leu Gly Trp Pro Leu 180 185 190	576
tac tta gct ttc aat gtc tct ggt aga cct tac gat cgc ttt gct tgc Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Arg Phe Ala Cys 195 200 205	624
cat tat gat ccc tat ggc cca ata ttt tcc gaa aga gaa agg ctt cag His Tyr Asp Pro Tyr Gly Pro Ile Phe Ser Glu Arg Glu Arg Leu Gln 210 215 220	672
att tac att gct gac ctc gga atc ttt gcc aca acg ttt gtg ctt tat Ile Tyr Ile Ala Asp Leu Gly Ile Phe Ala Thr Thr Phe Val Leu Tyr 225 230 235 240	720
cag gct aca atg gca aaa ggg ttg gct tgg gta atg cgt atc tat ggg	768

Gln Ala Thr Met Ala Lys Gly Leu Ala Trp Val Met Arg Ile Tyr Gly			
245	250	255	
gtg cca ttg ctt att gtt aac tgt ttc ctt gtt atg atc aca tac ttg	816		
Val Pro Leu Leu Ile Val Asn Cys Phe Leu Val Met Ile Thr Tyr Leu			
260	265	270	
cag cac act cac cca gct att cca cgc tat ggc tca tcg gaa tgg gat	864		
Gln His Thr His Pro Ala Ile Pro Arg Tyr Gly Ser Ser Glu Trp Asp			
275	280	285	
tgg ctc cgg gga gca atg gtg act gtc gat aga gat tat ggg gtg ttg	912		
Trp Leu Arg Gly Ala Met Val Thr Val Asp Arg Asp Tyr Gly Val Leu			
290	295	300	
aat aaa gta ttc cat aac att gca gac act cat gta gct cat cat ctc	960		
Asn Lys Val Phe His Asn Ile Ala Asp Thr His Val Ala His His Leu			
305	310	315	320
ttt gct aca gtg cca cat tac cat gca atg gag gcc act aaa gca atc	1008		
Phe Ala Thr Val Pro His Tyr His Ala Met Glu Ala Thr Lys Ala Ile			
325	330	335	
aag cct ata atg ggt gag tat tac cgg tat gat ggt acc cca ttt tac	1056		
Lys Pro Ile Met Gly Glu Tyr Tyr Arg Tyr Asp Gly Thr Pro Phe Tyr			
340	345	350	
aag gca ttg tgg agg gag gca aag gag tgc ttg ttc gtc gag cca gat	1104		
Lys Ala Leu Trp Arg Glu Ala Lys Glu Cys Leu Phe Val Glu Pro Asp			
355	360	365	
gaa gga gct cct aca caa ggc gtt ttc tgg tac cgg aac aag tat	1149		
Glu Gly Ala Pro Thr Gln Gly Val Phe Trp Tyr Arg Asn Lys Tyr			
370	375	380	
taa	1152		
<210> 8			
<211> 1155			
<212> DNA			
<213> <i>Lesquerella fendleri</i>			
<220>			
<221> CDS			
<222> (1)...(1152)			
<400> 8			
atg ggt gca ggt gga aga atg ccg gtt cct act tct tcc aag aaa tcg	48		
Met Gly Ala Gly Gly Arg Met Pro Val Pro Thr Ser Ser Lys Lys Ser			
1	5	10	15
gaa acc gac acc aca aag cgt gtg ccg tgc gag aaa ccg cct ttc tcg	96		
Glu Thr Asp Thr Thr Lys Arg Val Pro Cys Glu Lys Pro Pro Phe Ser			
20	25	30	
gtg gga gat ctg aag aaa gca atc cca cag cat tgt ttt cag cgc tct	144		
Val Gly Asp Leu Lys Lys Ala Ile Pro Gln His Cys Phe Gln Arg Ser			

atc cct cgt tct ttc tcc tac ctt ctc aca gat atc act tta gtt tct	192
Ile Pro Arg Ser Phe Ser Tyr Leu Leu Thr Asp Ile Thr Leu Val Ser	
50 55 60	
tgc ttc tac tac gtt gcc aca aat tac ttc tct ctt ctt cct cag cct	240
Cys Phe Tyr Tyr Val Ala Thr Asn Tyr Phe Ser Leu Leu Pro Gln Pro	
65 70 75 80	
ctc tct act tac cta gct tgg cct ctc tat tgg gta tgt caa ggc tgt	288
Leu Ser Thr Tyr Leu Ala Trp Pro Leu Tyr Trp Val Cys Gln Gly Cys	
85 90 95	
gtc tta aca ggt atc tgg gtc att ggc cat gaa tgt ggt cac cat gca	336
Val Leu Thr Gly Ile Trp Val Ile Gly His Glu Cys Gly His His Ala	
100 105 110	
ttc agt gac tat caa tgg gta gat gac act gtt ggt ttt atc ttc cat	384
Phe Ser Asp Tyr Gln Trp Val Asp Asp Thr Val Gly Phe Ile Phe His	
115 120 125	
tcc ttc ctt ctc gtc cct tac ttc tcc tgg aaa tac agt cat cgt cgt	432
Ser Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg	
130 135 140	
cac cat tcc aac aat gga tct ctc gag aaa gat gaa gtc ttt gtc cca	480
His His Ser Asn Asn Gly Ser Leu Glu Lys Asp Glu Val Phe Val Pro	
145 150 155 160	
ccg aaa aaa gct gca gtc aaa tgg tat gtt aaa tac ctc aac aac cct	528
Pro Lys Lys Ala Ala Val Lys Trp Tyr Val Lys Tyr Leu Asn Asn Pro	
165 170 175	
ctt gga cgc att ctg gtg tta aca gtt cag ttt atc ctc ggg tgg cct	576
Leu Gly Arg Ile Leu Val Leu Thr Val Gln Phe Ile Leu Gly Trp Pro	
180 185 190	
ttg tat cta ccc ttt aat gta tca ggt aga cct tat gat ggt ttc gct	624
Leu Tyr Leu Pro Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Phe Ala	
195 200 205	
tca cat ttc ttc cct cat gca cct atc ttt aaa gac cgc gaa cgt ctc	672
Ser His Phe Phe Pro His Ala Pro Ile Phe Lys Asp Arg Glu Arg Leu	
210 215 220	
cag ata tac atc tca gat gct ggt att cta gct gtc tgt tat ggt ctt	720
Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu	
225 230 235 240	
tac cgt tac gct gct tca caa gga ttg act gct atg atc tgc gtc tat	768
Tyr Arg Tyr Ala Ala Ser Gln Gly Leu Thr Ala Met Ile Cys Val Tyr	
245 250 255	
gga gta ccg ctt ttg ata gtg aac ttt ttc ctt gtc ttg gta act ttc	816
Gly Val Pro Leu Leu Ile Val Asn Phe Phe Leu Val Leu Val Thr Phe	
260 265 270	

ttg cag cac act cat cct tcg tta cct cac tat gat tca acc gag tgg	864
Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Thr Glu Trp	
275 280 285	
gaa tgg att aga gga gct ttg gtt acg gta gac aga gac tat gga atc	912
Glu Trp Ile Arg Gly Ala Leu Val Thr Val Asp Arg Asp Tyr Gly Ile	
290 295 300	
ttg aac aag gtg ttt cac aac ata aca gac aca cat gtg gct cat cat	960
Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His	
305 310 315 320	
ctc ttt gca act ata ccg cat tat aac gca atg gaa gct aca gag gcg	1008
Leu Phe Ala Thr Ile Pro His Tyr Asn Ala Met Glu Ala Thr Glu Ala	
325 330 335	
ata aag cca ata ctt ggt gat tac tac cac ttc gat gga aca ccg tgg	1056
Ile Lys Pro Ile Leu Gly Asp Tyr Tyr His Phe Asp Gly Thr Pro Trp	
340 345 350	
tat gtg gcc atg tat agg gaa gca aag gag tgt ctc tat gta gaa ccg	1104
Tyr Val Ala Met Tyr Arg Glu Ala Lys Glu Cys Leu Tyr Val Glu Pro	
355 360 365	
gat acg gaa cgt ggg aag aaa ggt gtg tac tat tac aac aat aag tta	1152
Asp Thr Glu Arg Gly Lys Lys Gly Val Tyr Tyr Tyr Asn Asn Lys Leu	
370 375 380	
tga	1155
<210> 9	
<211> 1152	
<212> DNA	
<213> <i>Lesquerella lindheimeri</i>	
<220>	
<221> CDS	
<222> (1)...(1149)	
<400> 9	
atg ggt gca ggt gga aga atg ccg gtt cct act tct tcc aag aaa tcg	48
Met Gly Ala Gly Gly Arg Met Pro Val Pro Thr Ser Ser Lys Lys Ser	
1 5 10 15	
gaa acc gac acc aca aag cgt gtg ccg tgc gag aaa ccg cct ttc tcg	96
Glu Thr Asp Thr Thr Lys Arg Val Pro Cys Glu Lys Pro Pro Phe Ser	
20 25 30	
gtg gga gat cta agg aaa gca atc cca cgg cat tgt ttc aaa cgc tct	144
Val Gly Asp Leu Arg Lys Ala Ile Pro Arg His Cys Phe Lys Arg Ser	
35 40 45	
atc cct cgt tct ttc tcc tat ctt ctc aca gat atc att tta gct tct	192
Ile Pro Arg Ser Phe Ser Tyr Leu Leu Thr Asp Ile Ile Leu Ala Ser	
50 55 60	



tgc ttc tac tac gtg gcc acc aat tac ttc tca ctt ctt cca cag cct	240
Cys Phe Tyr Tyr Val Ala Thr Asn Tyr Phe Ser Leu Leu Pro Gln Pro	
65 70 75 80	
ctc tct act tac ttt gct tgg cct ctc tat tgg gta tgt caa ggc tgt	288
Leu Ser Thr Tyr Phe Ala Trp Pro Leu Tyr Trp Val Cys Gln Gly Cys	
85 90 95	
gtc tta acc ggt gtt tgg gtc ctt ggc cat gaa tgt ggt cac caa gca	336
Val Leu Thr Gly Val Trp Val Leu Gly His Glu Cys Gly His Gln Ala	
100 105 110	
ttt agt gac tat caa tgg gta gat gac act gtt ggt ttt atc atc cat	384
Phe Ser Asp Tyr Gln Trp Val Asp Asp Thr Val Gly Phe Ile Ile His	
115 120 125	
acc ttc ctc ctc atc cct tac ttc tcc tgg aag tat agt cat cgt cgt	432
Thr Phe Leu Leu Ile Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg	
130 135 140	
cac cat gcc aat aat gga tca ctc gag aga gat gaa gtc ttt gtc cca	480
His His Ala Asn Asn Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro	
145 150 155 160	
ccg aag aaa gct gca gtc aaa tgg tat gtc aaa tac ctc aac aac cct	528
Pro Lys Lys Ala Ala Val Lys Trp Tyr Val Lys Tyr Leu Asn Asn Pro	
165 170 175	
ctt gga cgc act gtg gtg tta ata gtc cag ttt gtc ctc gga tgg ccc	576
Leu Gly Arg Thr Val Val Leu Ile Val Gln Phe Val Leu Gly Trp Pro	
180 185 190	
ttg tac cta gcc ttt aac gta tca ggt aga tcc tat gat ggt ttc gct	624
Leu Tyr Leu Ala Phe Asn Val Ser Gly Arg Ser Tyr Asp Gly Phe Ala	
195 200 205	
tca cat ttc ttc cca cat gca ccc atc ttc aag gac cga gaa cgt ctc	672
Ser His Phe Phe Pro His Ala Pro Ile Phe Lys Asp Arg Glu Arg Leu	
210 215 220	
cat ata tac atc aca gat gct ggt att cta gct gtc tgt tat ggt ctt	720
His Ile Tyr Ile Thr Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu	
225 230 235 240	
tac cgt tac gca gct aca aaa gga ttg acc gct atg atc tgc gtc tat	768
Tyr Arg Tyr Ala Ala Thr Lys Gly Leu Thr Ala Met Ile Cys Val Tyr	
245 250 255	
ggg gta cct cct ctg gtt gta aac ttt ttc ctt gtc ttg gtc act ttc	816
Gly Val Pro Pro Leu Val Val Asn Phe Phe Leu Val Leu Val Thr Phe	
260 265 270	
ttg cag cac act cat cct tca tta cct cac tat gat tca acc gag tgg	864
Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Thr Glu Trp	
275 280 285	
gac tgg att aga gga gcc atg gtt aca gta gac aga gac tat ggg atc	912

```

Asp Trp Ile Arg Gly Ala Met Val Thr Val Asp Arg Asp Tyr Gly Ile
 290                               295                               300

ttg aac aag gtg ttc cac aac ata aca gac aca cat gtg gct cat cat      960
Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His
305                               310                               315                               320

ctt ttc gca aca ata ccg cat tat aat gca atg gaa gct aca gag gcg      1008
Leu Phe Ala Thr Ile Pro His Tyr Asn Ala Met Glu Ala Thr Glu Ala
                               325                               330                               335

ata aag cca ata ctc gga gac tac tac cat ttc gat gga aca ccc tgg      1056
Ile Lys Pro Ile Leu Gly Asp Tyr Tyr His Phe Asp Gly Thr Pro Trp
                               340                               345                               350

tat gtg gct atg tat agg gaa gca aag cag tgt ctc tat gta gaa cag      1104
Tyr Val Ala Met Tyr Arg Glu Ala Lys Gln Cys Leu Tyr Val Glu Gln
                               355                               360                               365

gat aca gaa aag aag aaa ggt gtc tac tat tac aac aat aag tta      1149
Asp Thr Glu Lys Lys Lys Gly Val Tyr Tyr Tyr Asn Asn Lys Leu
                               370                               375                               380

tga                                                                    1152

<210> 10
<211> 1155
<212> DNA
<213> Lesquerella gracilis A

<220>
<221> CDS
<222> (1)...(1152)

<400> 10
atg ggt gca ggt gga aga atg ccg gtt cct act tct tcc aag aaa tcg      48
Met Gly Ala Gly Gly Arg Met Pro Val Pro Thr Ser Ser Lys Lys Ser
 1                               5                               10                               15

gaa acc gac acc aca aag cgt gtg ccg tgc gag aaa ccg cct ttc tcg      96
Glu Thr Asp Thr Thr Lys Arg Val Pro Cys Glu Lys Pro Pro Phe Ser
                               20                               25                               30

gtg gga gat ctg aag aaa gca atc cca ccg cat tgt ttc aaa cgc tct      144
Val Gly Asp Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser
                               35                               40                               45

atc cct cgc tct ttc tct tac ctt ctc aca gat ttc att cta gct tct      192
Ile Pro Arg Ser Phe Ser Tyr Leu Leu Thr Asp Phe Ile Leu Ala Ser
                               50                               55                               60

tgc ttc tac tac gtg gct aca aat tac ttc tct ctt ctc cca cag cct      240
Cys Phe Tyr Tyr Val Ala Thr Asn Tyr Phe Ser Leu Leu Pro Gln Pro
 65                               70                               75                               80

gtc tct aat tac ctg gct tgg cct ctc tat tgg ata tgt caa ggc tgt      288
Val Ser Asn Tyr Leu Ala Trp Pro Leu Tyr Trp Ile Cys Gln Gly Cys

```

					85						90						95	
gtc	tta	acc	ggt	ggt	tgg	gtc	ctt	ggc	cat	gaa	tgt	ggt	cac	cat	gca	336		
Val	Leu	Thr	Gly	Val	Trp	Val	Leu	Gly	His	Glu	Cys	Gly	His	His	Ala			
					100						105						110	
ttc	agt	gac	tat	caa	tgg	gta	gat	gac	act	gtt	ggt	ttt	atc	atc	cat	384		
Phe	Ser	Asp	Tyr	Gln	Trp	Val	Asp	Asp	Thr	Val	Gly	Phe	Ile	Ile	His			
					115						120						125	
tcc	ttc	ctc	ctt	gtc	cct	tac	ttc	tcc	tgg	aag	tac	agt	cat	cgt	cgt	432		
Ser	Phe	Leu	Leu	Val	Pro	Tyr	Phe	Ser	Trp	Lys	Tyr	Ser	His	Arg	Arg			
					130						135						140	
cac	cat	tcc	aac	aat	gga	tcc	ctc	gag	aaa	gat	gaa	gtc	ttt	gtt	cca	480		
His	His	Ser	Asn	Asn	Gly	Ser	Leu	Glu	Lys	Asp	Glu	Val	Phe	Val	Pro			
					145						150						155	
cct	aag	aaa	gct	gca	gtc	aaa	tgg	tat	gtt	aag	tac	ctc	aac	aac	cct	528		
Pro	Lys	Lys	Ala	Ala	Val	Lys	Trp	Tyr	Val	Lys	Tyr	Leu	Asn	Asn	Pro			
					165						170						175	
ctt	gga	cgc	act	gtg	gtg	tta	ata	gtc	cag	ttt	gtc	ctc	ggg	tgg	cct	576		
Leu	Gly	Arg	Thr	Val	Val	Leu	Ile	Val	Gln	Phe	Val	Leu	Gly	Trp	Pro			
					180						185						190	
ttg	tat	cta	gcc	ttt	aac	gta	tca	ggt	aga	ccc	tat	gat	ggg	ttc	gct	624		
Leu	Tyr	Leu	Ala	Phe	Asn	Val	Ser	Gly	Arg	Pro	Tyr	Asp	Gly	Phe	Ala			
					195						200						205	
tca	cac	ttc	ttt	cct	cat	gca	ccc	atc	ttc	agg	gac	cgt	gaa	cgc	ctc	672		
Ser	His	Phe	Phe	Pro	His	Ala	Pro	Ile	Phe	Arg	Asp	Arg	Glu	Arg	Leu			
					210						215						220	
cat	ata	tac	atc	aca	gat	gct	ggt	att	cta	gct	gtc	tgt	tat	ggt	ctt	720		
His	Ile	Tyr	Ile	Thr	Asp	Ala	Gly	Ile	Leu	Ala	Val	Cys	Tyr	Gly	Leu			
					225						230						235	
tac	cgt	tac	gct	gct	tca	aaa	gga	ttg	acc	gct	atg	atc	tgc	gtc	tac	768		
Tyr	Arg	Tyr	Ala	Ala	Ser	Lys	Gly	Leu	Thr	Ala	Met	Ile	Cys	Val	Tyr			
					245						250						255	
gga	gta	ccg	ctt	ttg	ata	gtg	aac	ttt	ttc	ctc	gtg	ttg	gtc	act	ttc	816		
Gly	Val	Pro	Leu	Leu	Ile	Val	Asn	Phe	Phe	Leu	Val	Leu	Val	Thr	Phe			
					260						265						270	
ttg	cag	cac	act	cat	cct	tca	tta	cct	cac	tat	gat	tca	acc	gag	tgg	864		
Leu	Gln	His	Thr	His	Pro	Ser	Leu	Pro	His	Tyr	Asp	Ser	Thr	Glu	Trp			
					275						280						285	
gaa	tgg	att	aga	gga	gcc	ttg	gtt	aca	gta	gac	aga	gac	tat	gga	atc	912		
Glu	Trp	Ile	Arg	Gly	Ala	Leu	Val	Thr	Val	Asp	Arg	Asp	Tyr	Gly	Ile			
					290						295						300	
ttg	aac	aag	gtg	ttc	cac	aac	ata	aca	gac	aca	cat	gtg	gct	cat	cat	960		
Leu	Asn	Lys	Val	Phe	His	Asn	Ile	Thr	Asp	Thr	His	Val	Ala	His	His			
					305						310						315	
																	320	

```

att ttc gca aca ata ccg cat tat aat gca atg gaa gct aca gag gcg      1008
Ile Phe Ala Thr Ile Pro His Tyr Asn Ala Met Glu Ala Thr Glu Ala
                325                          330                          335

ata aag cca ata ctc gga gac tac tac cat ttc gat gga aca ccg tgg      1056
Ile Lys Pro Ile Leu Gly Asp Tyr Tyr His Phe Asp Gly Thr Pro Trp
                340                          345                          350

tat gtg gcc atg tac agg gaa gca aag gag tgt ctc tat gta gaa cag      1104
Tyr Val Ala Met Tyr Arg Glu Ala Lys Glu Cys Leu Tyr Val Glu Gln
                355                          360                          365

gat aca gaa cgt ggg aag aaa ggt gtc tac tat tac aac aat aag tta      1152
Asp Thr Glu Arg Gly Lys Lys Gly Val Tyr Tyr Tyr Asn Asn Lys Leu
                370                          375                          380

tga                                                                    1155

<210> 11
<211> 1155
<212> DNA
<213> Lesquerella gracilis B

<220>
<221> CDS
<222> (1)...(1152)

<400> 11
atg ggt gca ggt gga aga atg ccg gtt cct act tct tcc aag aaa tcg      48
Met Gly Ala Gly Gly Arg Met Pro Val Pro Thr Ser Ser Lys Lys Ser
  1                5                10                15

gaa acc gac acc aca aag cgt gtg ccg tgc gag aaa ccg cct ttc tcg      96
Glu Thr Asp Thr Thr Lys Arg Val Pro Cys Glu Lys Pro Pro Phe Ser
                20                25                30

gtg gga gat ctg aag aaa gca atc cca cag cat tgt ttt caa cgc tct      144
Val Gly Asp Leu Lys Lys Ala Ile Pro Gln His Cys Phe Gln Arg Ser
                35                40                45

atc cct cgt tct ttc tcc tac ctt ctc aca gat atc act tta gtt tct      192
Ile Pro Arg Ser Phe Ser Tyr Leu Leu Thr Asp Ile Thr Leu Val Ser
                50                55                60

tgc ttc tac tac gtt gcc aca aat tac ttc tct ctt ctt cct cag cct      240
Cys Phe Tyr Tyr Val Ala Thr Asn Tyr Phe Ser Leu Leu Pro Gln Pro
  65                70                75                80

ctc tct act tac cta gct tgg cct ctc tat tgg gta tgt caa ggc tgt      288
Leu Ser Thr Tyr Leu Ala Trp Pro Leu Tyr Trp Val Cys Gln Gly Cys
                85                90                95

gtc cta aca ggt atc tgg gtc ctt ggc cat gaa tgt ggt cac cat gca      336
Val Leu Thr Gly Ile Trp Val Leu Gly His Glu Cys Gly His His Ala
                100                105                110

```

ttc agt gac tat caa tgg cta gat gac act gtt ggt ttt atc ttc cat	384
Phe Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Phe Ile Phe His	
115 120 125	
tcc tta ctt ctc gtc cct tac ttc tcc tgg aaa tac agt cat cgt cgt	432
Ser Leu Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg	
130 135 140	
cac cat tcc aac aat gga tct ctc gag aaa gat gaa gtc ttt gtc cca	480
His His Ser Asn Asn Gly Ser Leu Glu Lys Asp Glu Val Phe Val Pro	
145 150 155 160	
ccg aaa aaa gct gca gtc aaa tgg tat gtt aaa tac ctc aac aac cct	528
Pro Lys Lys Ala Ala Val Lys Trp Tyr Val Lys Tyr Leu Asn Asn Pro	
165 170 175	
ctt gga cgc att ctg gtg tta aca gtt cgg ttt atc ctc ggg tgg cct	576
Leu Gly Arg Ile Leu Val Leu Thr Val Arg Phe Ile Leu Gly Trp Pro	
180 185 190	
ttg tat cta gcc ttt aat gta tca ggt aga cct tat gat ggt ttc gct	624
Leu Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Phe Ala	
195 200 205	
tca cat ttc ttc cct cat gca cct atc ttt aaa gac cgc gaa cgt ctc	672
Ser His Phe Phe Pro His Ala Pro Ile Phe Lys Asp Arg Glu Arg Leu	
210 215 220	
cag ata tac atc tca gat gct ggt att cta gct gtc tgt tat ggt ctt	720
Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu	
225 230 235 240	
tac cgt tac gct gct tca caa gga ttg acc gct atg atc tgc gtc tat	768
Tyr Arg Tyr Ala Ala Ser Gln Gly Leu Thr Ala Met Ile Cys Val Tyr	
245 250 255	
gga gta ccg ctt ttg ata gtg aac ttt ttc ctt gtc ttg gta act ttc	816
Gly Val Pro Leu Leu Ile Val Asn Phe Phe Leu Val Leu Val Thr Phe	
260 265 270	
ttg cag cac act cat cct tcg tta cct cac tat gat tca acc gag tgg	864
Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Thr Glu Trp	
275 280 285	
gaa tgg att aga gga gct ttg gtt acg gta gac aga gac tac gga atc	912
Glu Trp Ile Arg Gly Ala Leu Val Thr Val Asp Arg Asp Tyr Gly Ile	
290 295 300	
ttg aac aag gtg ttt cac aac ata aca gac aca cat gtg gct cat cat	960
Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His	
305 310 315 320	
ctt ttc gca act ata ccg cat tat aac gca atg gaa gct aca gag gcg	1008
Leu Phe Ala Thr Ile Pro His Tyr Asn Ala Met Glu Ala Thr Glu Ala	
325 330 335	
ata aag cca ata ctt ggt gat tac tac cat ttc gat gga aca ccg tgg	1056

Ile Lys Pro Ile Leu Gly Asp Tyr Tyr His Phe Asp Gly Thr Pro Trp	
340	345
350	
tat gtg gct atg tat agg gaa gca aag gag tgt ctc tat gta gaa ccg	1104
Tyr Val Ala Met Tyr Arg Glu Ala Lys Glu Cys Leu Tyr Val Glu Pro	
355	360
365	
gat acg gaa cgt ggg aag aaa ggt gtc tac tat tac aac aat aag tta	1152
Asp Thr Glu Arg Gly Lys Lys Gly Val Tyr Tyr Tyr Asn Asn Lys Leu	
370	375
380	
tga	1155
<210> 12	
<211> 1143	
<212> DNA	
<213> Crepis biennis	
<220>	
<221> CDS	
<222> (1)...(1140)	
<400> 12	
atg ggt gca ggt gga aga atg ccg gtt cct act tct tcc aag aaa tcg	48
Met Gly Ala Gly Gly Arg Met Pro Val Pro Thr Ser Ser Lys Lys Ser	
1	5
10	15
gaa acc gac acc aca aag cgt gtg ccg tgc gag aaa ccg cct ttc tcg	96
Glu Thr Asp Thr Thr Lys Arg Val Pro Cys Glu Lys Pro Pro Phe Ser	
20	25
30	
gtg gga gat ctg aag aaa gca atc cct ccc cat tgc ttc cag cga tct	144
Val Gly Asp Leu Lys Lys Ala Ile Pro Pro His Cys Phe Gln Arg Ser	
35	40
45	
gta atc cgt tca tct tac tat gta gtt cac gat ctc att att gcc tac	192
Val Ile Arg Ser Ser Tyr Tyr Val Val His Asp Leu Ile Ile Ala Tyr	
50	55
60	
atc ttc tac ttc ctt gcc gat aaa tat att ccg att ctc cct gct cct	240
Ile Phe Tyr Phe Leu Ala Asp Lys Tyr Ile Pro Ile Leu Pro Ala Pro	
65	70
75	80
cta gcc tac tta gct tgg ccc ctt tac tgg ttc tgt caa gct agc atc	288
Leu Ala Tyr Leu Ala Trp Pro Leu Tyr Trp Phe Cys Gln Ala Ser Ile	
85	90
95	
ctc act ggt tta tgg atc ctc ggt cat gaa tgc ggt cac cat gcc ttt	336
Leu Thr Gly Leu Trp Ile Leu Gly His Glu Cys Gly His His Ala Phe	
100	105
110	
agc gag cac caa tgg gtt gac gac act gtg ggc ttc atg gtc cac tca	384
Ser Glu His Gln Trp Val Asp Asp Thr Val Gly Phe Met Val His Ser	
115	120
125	
ttt ctc ctc acc ccg tat ttc tcg tgg aaa tac agt cac cgg aat cac	432
Phe Leu Leu Thr Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Asn His	

130		135		140		
cat gcc aac aca agt tcc att gat aac gat gaa gtt tac att ccg aaa						480
His Ala Asn Thr Ser Ser Ile Asp Asn Asp Glu Val Tyr Ile Pro Lys						
145		150		155		160
agc aag tcc aaa ctc gcg ctt acc tat aaa ctt ctt aac aac ccg cct						528
Ser Lys Ser Lys Leu Ala Leu Thr Tyr Lys Leu Leu Asn Asn Pro Pro						
		165		170		175
ggt cga ctg tta gtt atg gtt atc atg ttc acc cta gga ttt cct tta						576
Gly Arg Leu Leu Val Met Val Ile Met Phe Thr Leu Gly Phe Pro Leu						
		180		185		190
tac ctc ttg aca aat att tcc ggc aag aag tac gac agg ttt gcc aac						624
Tyr Leu Leu Thr Asn Ile Ser Gly Lys Lys Tyr Asp Arg Phe Ala Asn						
		195		200		205
cac ttc gac ccc atg agt cca att ttc aag gaa cgt gag cgg ttt cag						672
His Phe Asp Pro Met Ser Pro Ile Phe Lys Glu Arg Glu Arg Phe Gln						
		210		215		220
gtc ttg ctt tcg gat ctt ggc ctt ctt gct gtg ttt tat gga att aaa						720
Val Leu Leu Ser Asp Leu Gly Leu Leu Ala Val Phe Tyr Gly Ile Lys						
		225		230		240
gtt gct gta gca aag aaa gga gct gcg tgg gtg gcg tgt atg tat gga						768
Val Ala Val Ala Lys Lys Gly Ala Ala Trp Val Ala Cys Met Tyr Gly						
		245		250		255
gtt ccg atg cta ggc gta ttt acc ctt ttc gat atc atc acg tac ttg						816
Val Pro Met Leu Gly Val Phe Thr Leu Phe Asp Ile Ile Thr Tyr Leu						
		260		265		270
cac cac acc cat cag tcg tct cct cat tat gac tca act gaa tgg aac						864
His His Thr His Gln Ser Ser Pro His Tyr Asp Ser Thr Glu Trp Asn						
		275		280		285
tgg atc aga ggg gcg ttg tca gca atc gat agg gac ttt ggg ttc atg						912
Trp Ile Arg Gly Ala Leu Ser Ala Ile Asp Arg Asp Phe Gly Phe Met						
		290		295		300
aat agt gtt ttc cat gat gtt aca cac act cac gtc atg cat cat atg						960
Asn Ser Val Phe His Asp Val Thr His Thr His Val Met His His Met						
		305		310		315
ttt tca tac att cca cac tat cat gcg aaa gag gca agg gat gca atc						1008
Phe Ser Tyr Ile Pro His Tyr His Ala Lys Glu Ala Arg Asp Ala Ile						
		325		330		335
aat aca atc ata ggc gac tat tat atg atc gat agg act cca att ttg						1056
Asn Thr Ile Ile Gly Asp Tyr Tyr Met Ile Asp Arg Thr Pro Ile Leu						
		340		345		350
aaa gca ctg tgg aga gag gcc aag gaa tgc atg tac atc gag cct gat						1104
Lys Ala Leu Trp Arg Glu Ala Lys Glu Cys Met Tyr Ile Glu Pro Asp						
		355		360		365

agc aag cgc aaa ggt gtt tat tgg tat cat aaa ttg tga  
 Ser Lys Arg Lys Gly Val Tyr Trp Tyr His Lys Leu  
     370                                    375                                    380

1143

<210> 13  
 <211> 387  
 <212> PRT  
 <213> Ricinus communis

<400> 13

Met	Gly	Gly	Gly	Gly	Arg	Met	Ser	Thr	Val	Ile	Thr	Ser	Asn	Asn	Ser	1	5	10	15
Glu	Lys	Lys	Gly	Gly	Ser	Ser	His	Leu	Lys	Arg	Ala	Pro	His	Thr	Lys	20	25	30	
Pro	Pro	Phe	Thr	Leu	Gly	Asp	Leu	Lys	Arg	Ala	Ile	Pro	Pro	His	Cys	35	40	45	
Phe	Glu	Arg	Ser	Phe	Val	Arg	Ser	Phe	Ser	Tyr	Val	Ala	Tyr	Asp	Val	50	55	60	
Cys	Leu	Ser	Phe	Leu	Phe	Tyr	Ser	Ile	Ala	Thr	Asn	Phe	Phe	Pro	Tyr	65	70	75	80
Ile	Ser	Ser	Pro	Leu	Ser	Tyr	Val	Ala	Trp	Leu	Val	Tyr	Trp	Leu	Phe	85	90	95	
Gln	Gly	Cys	Ile	Leu	Thr	Gly	Leu	Trp	Val	Ile	Gly	His	Glu	Cys	Gly	100	105	110	
His	His	Ala	Phe	Ser	Glu	Tyr	Gln	Leu	Ala	Asp	Asp	Ile	Val	Gly	Leu	115	120	125	
Ile	Val	His	Ser	Ala	Leu	Leu	Val	Pro	Tyr	Phe	Ser	Trp	Lys	Tyr	Ser	130	135	140	
His	Arg	Arg	His	His	Ser	Asn	Ile	Gly	Ser	Leu	Glu	Arg	Asp	Glu	Val	145	150	155	160
Phe	Val	Pro	Lys	Ser	Lys	Ser	Lys	Ile	Ser	Trp	Tyr	Ser	Lys	Tyr	Leu	165	170	175	
Asn	Asn	Pro	Pro	Gly	Arg	Val	Leu	Thr	Leu	Ala	Ala	Thr	Leu	Leu	Leu	180	185	190	
Gly	Trp	Pro	Leu	Tyr	Leu	Ala	Phe	Asn	Val	Ser	Gly	Arg	Pro	Tyr	Asp	195	200	205	
Arg	Phe	Ala	Cys	His	Tyr	Asp	Pro	Tyr	Gly	Pro	Ile	Phe	Ser	Glu	Arg	210	215	220	
Glu	Arg	Leu	Gln	Ile	Tyr	Ile	Ala	Asp	Leu	Gly	Ile	Phe	Ala	Thr	Thr	225	230	235	240
Phe	Val	Leu	Tyr	Gln	Ala	Thr	Met	Ala	Lys	Gly	Leu	Ala	Trp	Val	Met	245	250	255	
Arg	Ile	Tyr	Gly	Val	Pro	Leu	Leu	Ile	Val	Asn	Cys	Phe	Leu	Val	Met	260	265	270	
Ile	Thr	Tyr	Leu	Gln	His	Thr	His	Pro	Ala	Ile	Pro	Arg	Tyr	Gly	Ser	275	280	285	
Ser	Glu	Trp	Asp	Trp	Leu	Arg	Gly	Ala	Met	Val	Thr	Val	Asp	Arg	Asp	290	295	300	
Tyr	Gly	Val	Leu	Asn	Lys	Val	Phe	His	Asn	Ile	Ala	Asp	Thr	His	Val	305	310	315	320
Ala	His	His	Leu	Phe	Ala	Thr	Val	Pro	His	Tyr	His	Ala	Met	Glu	Ala	325	330	335	
Thr	Lys	Ala	Ile	Lys	Pro	Ile	Met	Gly	Glu	Tyr	Tyr	Arg	Tyr	Asp	Gly	340	345	350	
Thr	Pro	Phe	Tyr	Lys	Ala	Leu	Trp	Arg	Glu	Ala	Lys	Glu	Cys	Leu	Phe	355	360	365	



Val Glu Pro Asp Glu Gly Ala Pro Thr Gln Gly Val Phe Trp Tyr Arg  
 370 375 380  
 Asn Lys Tyr  
 385

<210> 14  
 <211> 384  
 <212> PRT  
 <213> *Lesquerella fendleri*

<400> 14  
 Met Gly Ala Gly Gly Arg Ile Met Val Thr Pro Ser Ser Lys Lys Ser  
 1 5 10 15  
 Glu Thr Glu Ala Leu Lys Arg Gly Pro Cys Glu Lys Pro Pro Phe Thr  
 20 25 30  
 Val Lys Asp Leu Lys Lys Ala Ile Pro Gln His Cys Phe Gln Arg Ser  
 35 40 45  
 Ile Pro Arg Ser Phe Ser Tyr Leu Leu Thr Asp Ile Thr Leu Val Ser  
 50 55 60  
 Cys Phe Tyr Tyr Val Ala Thr Asn Tyr Phe Ser Leu Leu Pro Gln Pro  
 65 70 75 80  
 Leu Ser Thr Tyr Leu Ala Trp Pro Leu Tyr Trp Val Cys Gln Gly Cys  
 85 90 95  
 Val Leu Thr Gly Ile Trp Val Ile Gly His Glu Cys Gly His His Ala  
 100 105 110  
 Phe Ser Asp Tyr Gln Trp Val Asp Asp Thr Val Gly Phe Ile Phe His  
 115 120 125  
 Ser Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg  
 130 135 140  
 His His Ser Asn Asn Gly Ser Leu Glu Lys Asp Glu Val Phe Val Pro  
 145 150 155 160  
 Pro Lys Lys Ala Ala Val Lys Trp Tyr Val Lys Tyr Leu Asn Asn Pro  
 165 170 175  
 Leu Gly Arg Ile Leu Val Leu Thr Val Gln Phe Ile Leu Gly Trp Pro  
 180 185 190  
 Leu Tyr Leu Pro Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Phe Ala  
 195 200 205  
 Ser His Phe Phe Pro His Ala Pro Ile Phe Lys Asp Arg Glu Arg Leu  
 210 215 220  
 Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu  
 225 230 235 240  
 Tyr Arg Tyr Ala Ala Ser Gln Gly Leu Thr Ala Met Ile Cys Val Tyr  
 245 250 255  
 Gly Val Pro Leu Leu Ile Val Asn Phe Phe Leu Val Leu Val Thr Phe  
 260 265 270  
 Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Thr Glu Trp  
 275 280 285  
 Glu Trp Ile Arg Gly Ala Leu Val Thr Val Asp Arg Asp Tyr Gly Ile  
 290 295 300  
 Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His  
 305 310 315 320  
 Leu Phe Ala Thr Ile Pro His Tyr Asn Ala Met Glu Ala Thr Glu Ala  
 325 330 335  
 Ile Lys Pro Ile Leu Gly Asp Tyr Tyr His Phe Asp Gly Thr Pro Trp  
 340 345 350  
 Tyr Val Ala Met Tyr Arg Glu Ala Lys Glu Cys Leu Tyr Val Glu Pro  
 355 360 365

Asp Thr Glu Arg Gly Lys Lys Gly Val Tyr Tyr Tyr Asn Asn Lys Leu  
 370 375 380

<210> 15

<211> 383

<212> PRT

<213> *Lesquerella lindheimeri*

<400> 15

Met Gly Ala Gly Gly Arg Ile Met Val Thr Pro Ser Ser Lys Lys Ser  
 1 5 10 15  
 Lys Pro Glu Ala Leu Arg Arg Gly Pro Gly Glu Lys Pro Pro Phe Thr  
 20 25 30  
 Val Gln Asp Leu Arg Lys Ala Ile Pro Arg His Cys Phe Lys Arg Ser  
 35 40 45  
 Ile Pro Arg Ser Phe Ser Tyr Leu Leu Thr Asp Ile Ile Leu Ala Ser  
 50 55 60  
 Cys Phe Tyr Tyr Val Ala Thr Asn Tyr Phe Ser Leu Leu Pro Gln Pro  
 65 70 75 80  
 Leu Ser Thr Tyr Phe Ala Trp Pro Leu Tyr Trp Val Cys Gln Gly Cys  
 85 90 95  
 Val Leu Thr Gly Val Trp Val Leu Gly His Glu Cys Gly His Gln Ala  
 100 105 110  
 Phe Ser Asp Tyr Gln Trp Val Asp Asp Thr Val Gly Phe Ile Ile His  
 115 120 125  
 Thr Phe Leu Leu Ile Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg  
 130 135 140  
 His His Ala Asn Asn Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro  
 145 150 155 160  
 Pro Lys Lys Ala Ala Val Lys Trp Tyr Val Lys Tyr Leu Asn Asn Pro  
 165 170 175  
 Leu Gly Arg Thr Val Val Leu Ile Val Gln Phe Val Leu Gly Trp Pro  
 180 185 190  
 Leu Tyr Leu Ala Phe Asn Val Ser Gly Arg Ser Tyr Asp Gly Phe Ala  
 195 200 205  
 Ser His Phe Phe Pro His Ala Pro Ile Phe Lys Asp Arg Glu Arg Leu  
 210 215 220  
 His Ile Tyr Ile Thr Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu  
 225 230 235 240  
 Tyr Arg Tyr Ala Ala Thr Lys Gly Leu Thr Ala Met Ile Cys Val Tyr  
 245 250 255  
 Gly Val Pro Pro Leu Val Val Asn Phe Phe Leu Val Leu Val Thr Phe  
 260 265 270  
 Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Thr Glu Trp  
 275 280 285  
 Asp Trp Ile Arg Gly Ala Met Val Thr Val Asp Arg Asp Tyr Gly Ile  
 290 295 300  
 Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His  
 305 310 315 320  
 Leu Phe Ala Thr Ile Pro His Tyr Asn Ala Met Glu Ala Thr Glu Ala  
 325 330 335  
 Ile Lys Pro Ile Leu Gly Asp Tyr Tyr His Phe Asp Gly Thr Pro Trp  
 340 345 350  
 Tyr Val Ala Met Tyr Arg Glu Ala Lys Gln Cys Leu Tyr Val Glu Gln  
 355 360 365  
 Asp Thr Glu Lys Lys Lys Gly Val Tyr Tyr Tyr Asn Asn Lys Leu  
 370 375 380

<210> 16  
 <211> 384  
 <212> PRT  
 <213> *Lesquerella gracilis* A

<400> 16

Met	Gly	Ala	Gly	Gly	Arg	Ile	Met	Val	Thr	Pro	Ser	Ser	Lys	Lys	Ser
1				5					10					15	
Lys	Pro	Gln	Ala	Leu	Arg	Arg	Gly	Pro	Cys	Glu	Lys	Pro	Pro	Phe	Thr
			20					25					30		
Val	Lys	Asp	Leu	Lys	Lys	Ala	Ile	Pro	Pro	His	Cys	Phe	Lys	Arg	Ser
		35					40					45			
Ile	Pro	Arg	Ser	Phe	Ser	Tyr	Leu	Leu	Thr	Asp	Phe	Ile	Leu	Ala	Ser
		50				55					60				
Cys	Phe	Tyr	Tyr	Val	Ala	Thr	Asn	Tyr	Phe	Ser	Leu	Leu	Pro	Gln	Pro
65					70					75				80	
Val	Ser	Asn	Tyr	Leu	Ala	Trp	Pro	Leu	Tyr	Trp	Ile	Cys	Gln	Gly	Cys
				85					90					95	
Val	Leu	Thr	Gly	Val	Trp	Val	Leu	Gly	His	Glu	Cys	Gly	His	His	Ala
			100					105					110		
Phe	Ser	Asp	Tyr	Gln	Trp	Val	Asp	Asp	Thr	Val	Gly	Phe	Ile	Ile	His
		115					120					125			
Ser	Phe	Leu	Leu	Val	Pro	Tyr	Phe	Ser	Trp	Lys	Tyr	Ser	His	Arg	Arg
		130				135					140				
His	His	Ser	Asn	Asn	Gly	Ser	Leu	Glu	Lys	Asp	Glu	Val	Phe	Val	Pro
145					150					155				160	
Pro	Lys	Lys	Ala	Ala	Val	Lys	Trp	Tyr	Val	Lys	Tyr	Leu	Asn	Asn	Pro
				165						170				175	
Leu	Gly	Arg	Thr	Val	Val	Leu	Ile	Val	Gln	Phe	Val	Leu	Gly	Trp	Pro
			180					185					190		
Leu	Tyr	Leu	Ala	Phe	Asn	Val	Ser	Gly	Arg	Pro	Tyr	Asp	Gly	Phe	Ala
		195					200					205			
Ser	His	Phe	Phe	Pro	His	Ala	Pro	Ile	Phe	Arg	Asp	Arg	Glu	Arg	Leu
		210				215					220				
His	Ile	Tyr	Ile	Thr	Asp	Ala	Gly	Ile	Leu	Ala	Val	Cys	Tyr	Gly	Leu
225					230					235				240	
Tyr	Arg	Tyr	Ala	Ala	Ser	Lys	Gly	Leu	Thr	Ala	Met	Ile	Cys	Val	Tyr
				245					250					255	
Gly	Val	Pro	Leu	Leu	Ile	Val	Asn	Phe	Phe	Leu	Val	Leu	Val	Thr	Phe
			260					265					270		
Leu	Gln	His	Thr	His	Pro	Ser	Leu	Pro	His	Tyr	Asp	Ser	Thr	Glu	Trp
		275					280					285			
Glu	Trp	Ile	Arg	Gly	Ala	Leu	Val	Thr	Val	Asp	Arg	Asp	Tyr	Gly	Ile
	290					295					300				
Leu	Asn	Lys	Val	Phe	His	Asn	Ile	Thr	Asp	Thr	His	Val	Ala	His	His
305					310					315				320	
Ile	Phe	Ala	Thr	Ile	Pro	His	Tyr	Asn	Ala	Met	Glu	Ala	Thr	Glu	Ala
				325					330					335	
Ile	Lys	Pro	Ile	Leu	Gly	Asp	Tyr	Tyr	His	Phe	Asp	Gly	Thr	Pro	Trp
			340					345					350		
Tyr	Val	Ala	Met	Tyr	Arg	Glu	Ala	Lys	Glu	Cys	Leu	Tyr	Val	Glu	Gln
		355					360					365			
Asp	Thr	Glu	Arg	Gly	Lys	Lys	Gly	Val	Tyr	Tyr	Tyr	Asn	Asn	Lys	Leu
	370						375								380

<210> 17

<211> 384  
 <212> PRT  
 <213> *Lesquerella gracilis* B

<400> 17

Met	Gly	Ala	Gly	Gly	Arg	Ile	Met	Val	Thr	Pro	Ser	Ser	Lys	Lys	Ser
1				5					10					15	
Glu	Thr	Glu	Ala	Leu	Lys	Arg	Gly	Pro	Cys	Glu	Lys	Pro	Pro	Phe	Thr
			20					25					30		
Val	Lys	Asp	Leu	Lys	Lys	Ala	Ile	Pro	Gln	His	Cys	Phe	Gln	Arg	Ser
		35					40					45			
Ile	Pro	Arg	Ser	Phe	Ser	Tyr	Leu	Leu	Thr	Asp	Ile	Thr	Leu	Val	Ser
	50					55					60				
Cys	Phe	Tyr	Tyr	Val	Ala	Thr	Asn	Tyr	Phe	Ser	Leu	Leu	Pro	Gln	Pro
65					70					75					80
Leu	Ser	Thr	Tyr	Leu	Ala	Trp	Pro	Leu	Tyr	Trp	Val	Cys	Gln	Gly	Cys
				85					90					95	
Val	Leu	Thr	Gly	Ile	Trp	Val	Leu	Gly	His	Glu	Cys	Gly	His	His	Ala
			100					105					110		
Phe	Ser	Asp	Tyr	Gln	Trp	Leu	Asp	Asp	Thr	Val	Gly	Phe	Ile	Phe	His
		115					120					125			
Ser	Leu	Leu	Leu	Val	Pro	Tyr	Phe	Ser	Trp	Lys	Tyr	Ser	His	Arg	Arg
	130					135						140			
His	His	Ser	Asn	Asn	Gly	Ser	Leu	Glu	Lys	Asp	Glu	Val	Phe	Val	Pro
145					150					155					160
Pro	Lys	Lys	Ala	Ala	Val	Lys	Trp	Tyr	Val	Lys	Tyr	Leu	Asn	Asn	Pro
				165					170					175	
Leu	Gly	Arg	Ile	Leu	Val	Leu	Thr	Val	Arg	Phe	Ile	Leu	Gly	Trp	Pro
			180					185					190		
Leu	Tyr	Leu	Ala	Phe	Asn	Val	Ser	Gly	Arg	Pro	Tyr	Asp	Gly	Phe	Ala
	195						200					205			
Ser	His	Phe	Phe	Pro	His	Ala	Pro	Ile	Phe	Lys	Asp	Arg	Glu	Arg	Leu
	210					215					220				
Gln	Ile	Tyr	Ile	Ser	Asp	Ala	Gly	Ile	Leu	Ala	Val	Cys	Tyr	Gly	Leu
225					230					235					240
Tyr	Arg	Tyr	Ala	Ala	Ser	Gln	Gly	Leu	Thr	Ala	Met	Ile	Cys	Val	Tyr
				245					250					255	
Gly	Val	Pro	Leu	Leu	Ile	Val	Asn	Phe	Phe	Leu	Val	Leu	Val	Thr	Phe
			260					265					270		
Leu	Gln	His	Thr	His	Pro	Ser	Leu	Pro	His	Tyr	Asp	Ser	Thr	Glu	Trp
	275						280					285			
Glu	Trp	Ile	Arg	Gly	Ala	Leu	Val	Thr	Val	Asp	Arg	Asp	Tyr	Gly	Ile
	290					295				300					
Leu	Asn	Lys	Val	Phe	His	Asn	Ile	Thr	Asp	Thr	His	Val	Ala	His	His
305					310					315					320
Leu	Phe	Ala	Thr	Ile	Pro	His	Tyr	Asn	Ala	Met	Glu	Ala	Thr	Glu	Ala
				325					330					335	
Ile	Lys	Pro	Ile	Leu	Gly	Asp	Tyr	Tyr	His	Phe	Asp	Gly	Thr	Pro	Trp
			340					345					350		
Tyr	Val	Ala	Met	Tyr	Arg	Glu	Ala	Lys	Glu	Cys	Leu	Tyr	Val	Glu	Pro
		355					360					365			
Asp	Thr	Glu	Arg	Gly	Lys	Lys	Gly	Val	Tyr	Tyr	Tyr	Asn	Asn	Lys	Leu
	370					375						380			

<210> 18  
 <211> 374  
 <212> PRT

<213> *Crepis biennis*

&lt;400&gt; 18

Met Gly Ala His Gly His Gly Arg Thr Ser Lys Lys Ser Val Met Glu  
 1 5 10 15  
 Arg Val Ser Val Asp Pro Val Pro Phe Ser Leu Ser Asp Leu Lys Gln  
 20 25 30  
 Ala Ile Pro Pro His Cys Phe Gln Arg Ser Val Ile Arg Ser Ser Tyr  
 35 40 45  
 Tyr Val Val His Asp Leu Ile Ala Tyr Ile Phe Tyr Phe Leu Ala  
 50 55 60  
 Asp Lys Tyr Ile Pro Ile Leu Pro Ala Pro Leu Ala Tyr Leu Ala Trp  
 65 70 75 80  
 Pro Leu Tyr Trp Phe Cys Gln Ala Ser Ile Leu Thr Gly Leu Trp Ile  
 85 90 95  
 Leu Gly His Glu Cys Gly His His Ala Phe Ser Glu Tyr Gln Trp Val  
 100 105 110  
 Asp Asp Thr Val Gly Phe Met Val His Ser Phe Leu Leu Thr Pro Tyr  
 115 120 125  
 Phe Ser Trp Lys Tyr Ser His Arg Asn His His Ala Asn Thr Ser Ser  
 130 135 140  
 Ile Asp Asn Asp Glu Val Tyr Ile Pro Lys Ser Lys Ser Lys Leu Ala  
 145 150 155 160  
 Leu Thr Tyr Lys Leu Leu Asn Asn Pro Pro Gly Arg Leu Leu Val Met  
 165 170 175  
 Val Ile Met Phe Thr Leu Gly Phe Pro Leu Tyr Leu Leu Thr Asn Ile  
 180 185 190  
 Ser Gly Lys Lys Tyr Asp Arg Phe Ala Asn His Phe Asp Pro Met Ser  
 195 200 205  
 Pro Ile Phe Lys Glu Arg Glu Arg Phe Gln Val Leu Leu Ser Asp Leu  
 210 215 220  
 Gly Leu Leu Ala Val Phe Tyr Gly Ile Lys Val Ala Val Ala Lys Lys  
 225 230 235 240  
 Gly Ala Ala Trp Val Ala Cys Met Tyr Gly Val Pro Met Leu Gly Val  
 245 250 255  
 Phe Thr Leu Phe Asp Ile Ile Thr Tyr Leu His His Thr His Gln Ser  
 260 265 270  
 Ser Pro His Tyr Asp Ser Thr Glu Trp Asn Trp Ile Arg Gly Ala Leu  
 275 280 285  
 Ser Ala Ile Asp Arg Asp Phe Gly Phe Met Asn Ser Val Phe His Asp  
 290 295 300  
 Val Thr His Thr His Val Met His His Met Phe Ser Tyr Ile Pro His  
 305 310 315 320  
 Tyr His Ala Lys Glu Ala Arg Asp Ala Ile Asn Thr Ile Ile Gly Asp  
 325 330 335  
 Tyr Tyr Met Ile Asp Arg Thr Pro Ile Leu Lys Ala Leu Trp Arg Glu  
 340 345 350  
 Ala Lys Glu Cys Met Tyr Ile Glu Pro Asp Ser Lys Arg Lys Gly Val  
 355 360 365  
 Tyr Trp Tyr His Lys Leu  
 370

&lt;210&gt; 19

&lt;211&gt; 383

&lt;212&gt; PRT

<213> *Ricinus communis*

&lt;400&gt; 19

Met Gly Ala Gly Gly Arg Met Pro Val Pro Thr Ser Ser Lys Lys Ser  
 1 5 10 15  
 Glu Thr Asp Thr Thr Lys Arg Val Pro Cys Glu Lys Pro Pro Phe Ser  
 20 25 30  
 Val Gly Asp Leu Lys Lys Ala Ile Pro Pro His Cys Phe Glu Arg Ser  
 35 40 45  
 Phe Val Arg Ser Phe Ser Tyr Val Ala Tyr Asp Val Cys Leu Ser Phe  
 50 55 60  
 Leu Phe Tyr Ser Ile Ala Thr Asn Phe Phe Pro Tyr Ile Ser Ser Pro  
 65 70 75 80  
 Leu Ser Tyr Val Ala Trp Leu Val Tyr Trp Leu Phe Gln Gly Cys Ile  
 85 90 95  
 Leu Thr Gly Leu Trp Val Ile Gly His Glu Cys Gly His His Ala Phe  
 100 105 110  
 Ser Glu Tyr Gln Leu Ala Asp Asp Ile Val Gly Leu Ile Val His Ser  
 115 120 125  
 Ala Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg His  
 130 135 140  
 His Ser Asn Ile Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys  
 145 150 155 160  
 Ser Lys Ser Lys Ile Ser Trp Tyr Ser Lys Tyr Leu Asn Asn Pro Pro  
 165 170 175  
 Gly Arg Val Leu Thr Leu Ala Ala Thr Leu Leu Leu Gly Trp Pro Leu  
 180 185 190  
 Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Arg Phe Ala Cys  
 195 200 205  
 His Tyr Asp Pro Tyr Gly Pro Ile Phe Ser Glu Arg Glu Arg Leu Gln  
 210 215 220  
 Ile Tyr Ile Ala Asp Leu Gly Ile Phe Ala Thr Thr Phe Val Leu Tyr  
 225 230 235 240  
 Gln Ala Thr Met Ala Lys Gly Leu Ala Trp Val Met Arg Ile Tyr Gly  
 245 250 255  
 Val Pro Leu Leu Ile Val Asn Cys Phe Leu Val Met Ile Thr Tyr Leu  
 260 265 270  
 Gln His Thr His Pro Ala Ile Pro Arg Tyr Gly Ser Ser Glu Trp Asp  
 275 280 285  
 Trp Leu Arg Gly Ala Met Val Thr Val Asp Arg Asp Tyr Gly Val Leu  
 290 295 300  
 Asn Lys Val Phe His Asn Ile Ala Asp Thr His Val Ala His His Leu  
 305 310 315 320  
 Phe Ala Thr Val Pro His Tyr His Ala Met Glu Ala Thr Lys Ala Ile  
 325 330 335  
 Lys Pro Ile Met Gly Glu Tyr Tyr Arg Tyr Asp Gly Thr Pro Phe Tyr  
 340 345 350  
 Lys Ala Leu Trp Arg Glu Ala Lys Glu Cys Leu Phe Val Glu Pro Asp  
 355 360 365  
 Glu Gly Ala Pro Thr Gln Gly Val Phe Trp Tyr Arg Asn Lys Tyr  
 370 375 380

&lt;210&gt; 20

&lt;211&gt; 384

&lt;212&gt; PRT

<213> *Lesquerella fendleri*

&lt;400&gt; 20

Met Gly Ala Gly Gly Arg Met Pro Val Pro Thr Ser Ser Lys Lys Ser

1				5					10					15	
Glu	Thr	Asp	Thr	Thr	Lys	Arg	Val	Pro	Cys	Glu	Lys	Pro	Pro	Phe	Ser
				20				25					30		
Val	Gly	Asp	Leu	Lys	Lys	Ala	Ile	Pro	Gln	His	Cys	Phe	Gln	Arg	Ser
		35					40					45			
Ile	Pro	Arg	Ser	Phe	Ser	Tyr	Leu	Leu	Thr	Asp	Ile	Thr	Leu	Val	Ser
	50					55				60					
Cys	Phe	Tyr	Tyr	Val	Ala	Thr	Asn	Tyr	Phe	Ser	Leu	Leu	Pro	Gln	Pro
65					70					75					80
Leu	Ser	Thr	Tyr	Leu	Ala	Trp	Pro	Leu	Tyr	Trp	Val	Cys	Gln	Gly	Cys
				85					90					95	
Val	Leu	Thr	Gly	Ile	Trp	Val	Ile	Gly	His	Glu	Cys	Gly	His	His	Ala
			100					105					110		
Phe	Ser	Asp	Tyr	Gln	Trp	Val	Asp	Asp	Thr	Val	Gly	Phe	Ile	Phe	His
		115					120					125			
Ser	Phe	Leu	Leu	Val	Pro	Tyr	Phe	Ser	Trp	Lys	Tyr	Ser	His	Arg	Arg
	130					135					140				
His	His	Ser	Asn	Asn	Gly	Ser	Leu	Glu	Lys	Asp	Glu	Val	Phe	Val	Pro
145					150					155					160
Pro	Lys	Lys	Ala	Ala	Val	Lys	Trp	Tyr	Val	Lys	Tyr	Leu	Asn	Asn	Pro
			165					170						175	
Leu	Gly	Arg	Ile	Leu	Val	Leu	Thr	Val	Gln	Phe	Ile	Leu	Gly	Trp	Pro
			180					185					190		
Leu	Tyr	Leu	Pro	Phe	Asn	Val	Ser	Gly	Arg	Pro	Tyr	Asp	Gly	Phe	Ala
	195						200					205			
Ser	His	Phe	Phe	Pro	His	Ala	Pro	Ile	Phe	Lys	Asp	Arg	Glu	Arg	Leu
	210					215					220				
Gln	Ile	Tyr	Ile	Ser	Asp	Ala	Gly	Ile	Leu	Ala	Val	Cys	Tyr	Gly	Leu
225					230					235					240
Tyr	Arg	Tyr	Ala	Ala	Ser	Gln	Gly	Leu	Thr	Ala	Met	Ile	Cys	Val	Tyr
			245						250					255	
Gly	Val	Pro	Leu	Leu	Ile	Val	Asn	Phe	Phe	Leu	Val	Leu	Val	Thr	Phe
			260					265					270		
Leu	Gln	His	Thr	His	Pro	Ser	Leu	Pro	His	Tyr	Asp	Ser	Thr	Glu	Trp
	275						280					285			
Glu	Trp	Ile	Arg	Gly	Ala	Leu	Val	Thr	Val	Asp	Arg	Asp	Tyr	Gly	Ile
	290					295				300					
Leu	Asn	Lys	Val	Phe	His	Asn	Ile	Thr	Asp	Thr	His	Val	Ala	His	His
305					310				315						320
Leu	Phe	Ala	Thr	Ile	Pro	His	Tyr	Asn	Ala	Met	Glu	Ala	Thr	Glu	Ala
			325					330						335	
Ile	Lys	Pro	Ile	Leu	Gly	Asp	Tyr	Tyr	His	Phe	Asp	Gly	Thr	Pro	Trp
			340					345					350		
Tyr	Val	Ala	Met	Tyr	Arg	Glu	Ala	Lys	Glu	Cys	Leu	Tyr	Val	Glu	Pro
	355					360						365			
Asp	Thr	Glu	Arg	Gly	Lys	Lys	Gly	Val	Tyr	Tyr	Tyr	Asn	Asn	Lys	Leu
	370					375						380			

<210> 21

<211> 383

<212> PRT

<213> *Lesquerella lindheimeri*

<400> 21

Met	Gly	Ala	Gly	Gly	Arg	Met	Pro	Val	Pro	Thr	Ser	Ser	Lys	Lys	Ser
1				5					10					15	
Glu	Thr	Asp	Thr	Thr	Lys	Arg	Val	Pro	Cys	Glu	Lys	Pro	Pro	Phe	Ser

			20					25					30			
Val	Gly	Asp	Leu	Arg	Lys	Ala	Ile	Pro	Arg	His	Cys	Phe	Lys	Arg	Ser	
			35					40					45			
Ile	Pro	Arg	Ser	Phe	Ser	Tyr	Leu	Leu	Thr	Asp	Ile	Ile	Leu	Ala	Ser	
			50					55					60			
Cys	Phe	Tyr	Tyr	Val	Ala	Thr	Asn	Tyr	Phe	Ser	Leu	Leu	Pro	Gln	Pro	
65					70					75					80	
Leu	Ser	Thr	Tyr	Phe	Ala	Trp	Pro	Leu	Tyr	Trp	Val	Cys	Gln	Gly	Cys	
				85						90				95		
Val	Leu	Thr	Gly	Val	Trp	Val	Leu	Gly	His	Glu	Cys	Gly	His	Gln	Ala	
			100							105				110		
Phe	Ser	Asp	Tyr	Gln	Trp	Val	Asp	Asp	Thr	Val	Gly	Phe	Ile	Ile	His	
			115					120					125			
Thr	Phe	Leu	Leu	Ile	Pro	Tyr	Phe	Ser	Trp	Lys	Tyr	Ser	His	Arg	Arg	
			130					135					140			
His	His	Ala	Asn	Asn	Gly	Ser	Leu	Glu	Arg	Asp	Glu	Val	Phe	Val	Pro	
145					150					155					160	
Pro	Lys	Lys	Ala	Ala	Val	Lys	Trp	Tyr	Val	Lys	Tyr	Leu	Asn	Asn	Pro	
			165							170					175	
Leu	Gly	Arg	Thr	Val	Val	Leu	Ile	Val	Gln	Phe	Val	Leu	Gly	Trp	Pro	
			180						185					190		
Leu	Tyr	Leu	Ala	Phe	Asn	Val	Ser	Gly	Arg	Ser	Tyr	Asp	Gly	Phe	Ala	
			195					200					205			
Ser	His	Phe	Phe	Pro	His	Ala	Pro	Ile	Phe	Lys	Asp	Arg	Glu	Arg	Leu	
			210				215					220				
His	Ile	Tyr	Ile	Thr	Asp	Ala	Gly	Ile	Leu	Ala	Val	Cys	Tyr	Gly	Leu	
225					230					235					240	
Tyr	Arg	Tyr	Ala	Ala	Thr	Lys	Gly	Leu	Thr	Ala	Met	Ile	Cys	Val	Tyr	
			245							250				255		
Gly	Val	Pro	Pro	Leu	Val	Val	Asn	Phe	Phe	Leu	Val	Leu	Val	Thr	Phe	
			260						265					270		
Leu	Gln	His	Thr	His	Pro	Ser	Leu	Pro	His	Tyr	Asp	Ser	Thr	Glu	Trp	
			275					280					285			
Asp	Trp	Ile	Arg	Gly	Ala	Met	Val	Thr	Val	Asp	Arg	Asp	Tyr	Gly	Ile	
			290				295					300				
Leu	Asn	Lys	Val	Phe	His	Asn	Ile	Thr	Asp	Thr	His	Val	Ala	His	His	
305					310						315				320	
Leu	Phe	Ala	Thr	Ile	Pro	His	Tyr	Asn	Ala	Met	Glu	Ala	Thr	Glu	Ala	
			325							330				335		
Ile	Lys	Pro	Ile	Leu	Gly	Asp	Tyr	Tyr	His	Phe	Asp	Gly	Thr	Pro	Trp	
			340						345					350		
Tyr	Val	Ala	Met	Tyr	Arg	Glu	Ala	Lys	Gln	Cys	Leu	Tyr	Val	Glu	Gln	
			355					360					365			
Asp	Thr	Glu	Lys	Lys	Lys	Gly	Val	Tyr	Tyr	Tyr	Asn	Asn	Lys	Leu		
			370				375						380			

&lt;210&gt; 22

&lt;211&gt; 384

&lt;212&gt; PRT

<213> *Lesquerella gracilis* A

&lt;400&gt; 22

Met	Gly	Ala	Gly	Gly	Arg	Met	Pro	Val	Pro	Thr	Ser	Ser	Lys	Lys	Ser	
1				5					10					15		
Glu	Thr	Asp	Thr	Thr	Lys	Arg	Val	Pro	Cys	Glu	Lys	Pro	Pro	Phe	Ser	
			20					25					30			
Val	Gly	Asp	Leu	Lys	Lys	Ala	Ile	Pro	Pro	His	Cys	Phe	Lys	Arg	Ser	



		35					40					45			
Ile	Pro	Arg	Ser	Phe	Ser	Tyr	Leu	Leu	Thr	Asp	Phe	Ile	Leu	Ala	Ser
	50					55					60				
Cys	Phe	Tyr	Tyr	Val	Ala	Thr	Asn	Tyr	Phe	Ser	Leu	Leu	Pro	Gln	Pro
65					70					75					80
Val	Ser	Asn	Tyr	Leu	Ala	Trp	Pro	Leu	Tyr	Trp	Ile	Cys	Gln	Gly	Cys
				85					90					95	
Val	Leu	Thr	Gly	Val	Trp	Val	Leu	Gly	His	Glu	Cys	Gly	His	His	Ala
			100					105					110		
Phe	Ser	Asp	Tyr	Gln	Trp	Val	Asp	Asp	Thr	Val	Gly	Phe	Ile	Ile	His
		115					120					125			
Ser	Phe	Leu	Leu	Val	Pro	Tyr	Phe	Ser	Trp	Lys	Tyr	Ser	His	Arg	Arg
	130					135					140				
His	His	Ser	Asn	Asn	Gly	Ser	Leu	Glu	Lys	Asp	Glu	Val	Phe	Val	Pro
145					150					155					160
Pro	Lys	Lys	Ala	Ala	Val	Lys	Trp	Tyr	Val	Lys	Tyr	Leu	Asn	Asn	Pro
			165						170					175	
Leu	Gly	Arg	Thr	Val	Val	Leu	Ile	Val	Gln	Phe	Val	Leu	Gly	Trp	Pro
			180					185					190		
Leu	Tyr	Leu	Ala	Phe	Asn	Val	Ser	Gly	Arg	Pro	Tyr	Asp	Gly	Phe	Ala
	195						200					205			
Ser	His	Phe	Phe	Pro	His	Ala	Pro	Ile	Phe	Arg	Asp	Arg	Glu	Arg	Leu
	210					215					220				
His	Ile	Tyr	Ile	Thr	Asp	Ala	Gly	Ile	Leu	Ala	Val	Cys	Tyr	Gly	Leu
225					230					235					240
Tyr	Arg	Tyr	Ala	Ala	Ser	Lys	Gly	Leu	Thr	Ala	Met	Ile	Cys	Val	Tyr
			245						250					255	
Gly	Val	Pro	Leu	Leu	Ile	Val	Asn	Phe	Phe	Leu	Val	Leu	Val	Thr	Phe
			260					265					270		
Leu	Gln	His	Thr	His	Pro	Ser	Leu	Pro	His	Tyr	Asp	Ser	Thr	Glu	Trp
	275						280					285			
Glu	Trp	Ile	Arg	Gly	Ala	Leu	Val	Thr	Val	Asp	Arg	Asp	Tyr	Gly	Ile
	290					295					300				
Leu	Asn	Lys	Val	Phe	His	Asn	Ile	Thr	Asp	Thr	His	Val	Ala	His	His
305					310					315					320
Ile	Phe	Ala	Thr	Ile	Pro	His	Tyr	Asn	Ala	Met	Glu	Ala	Thr	Glu	Ala
			325						330					335	
Ile	Lys	Pro	Ile	Leu	Gly	Asp	Tyr	Tyr	His	Phe	Asp	Gly	Thr	Pro	Trp
			340					345					350		
Tyr	Val	Ala	Met	Tyr	Arg	Glu	Ala	Lys	Glu	Cys	Leu	Tyr	Val	Glu	Gln
	355						360					365			
Asp	Thr	Glu	Arg	Gly	Lys	Lys	Gly	Val	Tyr	Tyr	Tyr	Asn	Asn	Lys	Leu
	370					375						380			

&lt;210&gt; 23

&lt;211&gt; 384

&lt;212&gt; PRT

<213> *Lesquerella gracilis* B

&lt;400&gt; 23

Met	Gly	Ala	Gly	Gly	Arg	Met	Pro	Val	Pro	Thr	Ser	Ser	Lys	Lys	Ser
1				5					10					15	
Glu	Thr	Asp	Thr	Thr	Lys	Arg	Val	Pro	Cys	Glu	Lys	Pro	Pro	Phe	Ser
			20					25					30		
Val	Gly	Asp	Leu	Lys	Lys	Ala	Ile	Pro	Gln	His	Cys	Phe	Gln	Arg	Ser
		35				40						45			
Ile	Pro	Arg	Ser	Phe	Ser	Tyr	Leu	Leu	Thr	Asp	Ile	Thr	Leu	Val	Ser

50						55											60
Cys	Phe	Tyr	Tyr	Val	Ala	Thr	Asn	Tyr	Phe	Ser	Leu	Leu	Pro	Gln	Pro		
65					70					75					80		
Leu	Ser	Thr	Tyr	Leu	Ala	Trp	Pro	Leu	Tyr	Trp	Val	Cys	Gln	Gly	Cys		
				85					90					95			
Val	Leu	Thr	Gly	Ile	Trp	Val	Leu	Gly	His	Glu	Cys	Gly	His	His	Ala		
			100					105					110				
Phe	Ser	Asp	Tyr	Gln	Trp	Leu	Asp	Asp	Thr	Val	Gly	Phe	Ile	Phe	His		
		115					120					125					
Ser	Leu	Leu	Leu	Val	Pro	Tyr	Phe	Ser	Trp	Lys	Tyr	Ser	His	Arg	Arg		
	130					135						140					
His	His	Ser	Asn	Asn	Gly	Ser	Leu	Glu	Lys	Asp	Glu	Val	Phe	Val	Pro		
145				150						155					160		
Pro	Lys	Lys	Ala	Ala	Val	Lys	Trp	Tyr	Val	Lys	Tyr	Leu	Asn	Asn	Pro		
			165						170						175		
Leu	Gly	Arg	Ile	Leu	Val	Leu	Thr	Val	Arg	Phe	Ile	Leu	Gly	Trp	Pro		
			180					185						190			
Leu	Tyr	Leu	Ala	Phe	Asn	Val	Ser	Gly	Arg	Pro	Tyr	Asp	Gly	Phe	Ala		
		195					200						205				
Ser	His	Phe	Phe	Pro	His	Ala	Pro	Ile	Phe	Lys	Asp	Arg	Glu	Arg	Leu		
	210					215						220					
Gln	Ile	Tyr	Ile	Ser	Asp	Ala	Gly	Ile	Leu	Ala	Val	Cys	Tyr	Gly	Leu		
225					230					235					240		
Tyr	Arg	Tyr	Ala	Ala	Ser	Gln	Gly	Leu	Thr	Ala	Met	Ile	Cys	Val	Tyr		
			245						250					255			
Gly	Val	Pro	Leu	Leu	Ile	Val	Asn	Phe	Phe	Leu	Val	Leu	Val	Thr	Phe		
			260					265						270			
Leu	Gln	His	Thr	His	Pro	Ser	Leu	Pro	His	Tyr	Asp	Ser	Thr	Glu	Trp		
		275					280						285				
Glu	Trp	Ile	Arg	Gly	Ala	Leu	Val	Thr	Val	Asp	Arg	Asp	Tyr	Gly	Ile		
	290					295					300						
Leu	Asn	Lys	Val	Phe	His	Asn	Ile	Thr	Asp	Thr	His	Val	Ala	His	His		
305					310					315					320		
Leu	Phe	Ala	Thr	Ile	Pro	His	Tyr	Asn	Ala	Met	Glu	Ala	Thr	Glu	Ala		
			325						330					335			
Ile	Lys	Pro	Ile	Leu	Gly	Asp	Tyr	Tyr	His	Phe	Asp	Gly	Thr	Pro	Trp		
		340						345					350				
Tyr	Val	Ala	Met	Tyr	Arg	Glu	Ala	Lys	Glu	Cys	Leu	Tyr	Val	Glu	Pro		
		355					360						365				
Asp	Thr	Glu	Arg	Gly	Lys	Lys	Gly	Val	Tyr	Tyr	Tyr	Asn	Asn	Lys	Leu		
	370					375						380					

&lt;210&gt; 24

&lt;211&gt; 380

&lt;212&gt; PRT

&lt;213&gt; Crepis biennis

&lt;400&gt; 24

Met	Gly	Ala	Gly	Gly	Arg	Met	Pro	Val	Pro	Thr	Ser	Ser	Lys	Lys	Ser		
1				5					10					15			
Glu	Thr	Asp	Thr	Thr	Lys	Arg	Val	Pro	Cys	Glu	Lys	Pro	Pro	Phe	Ser		
			20					25					30				
Val	Gly	Asp	Leu	Lys	Lys	Ala	Ile	Pro	Pro	His	Cys	Phe	Gln	Arg	Ser		
		35					40					45					
Val	Ile	Arg	Ser	Ser	Tyr	Tyr	Val	Val	His	Asp	Leu	Ile	Ile	Ala	Tyr		
	50					55					60						
Ile	Phe	Tyr	Phe	Leu	Ala	Asp	Lys	Tyr	Ile	Pro	Ile	Leu	Pro	Ala	Pro		

65					70					75					80
Leu	Ala	Tyr	Leu	Ala	Trp	Pro	Leu	Tyr	Trp	Phe	Cys	Gln	Ala	Ser	Ile
				85					90					95	
Leu	Thr	Gly	Leu	Trp	Ile	Leu	Gly	His	Glu	Cys	Gly	His	His	Ala	Phe
			100					105					110		
Ser	Glu	His	Gln	Trp	Val	Asp	Asp	Thr	Val	Gly	Phe	Met	Val	His	Ser
		115					120					125			
Phe	Leu	Leu	Thr	Pro	Tyr	Phe	Ser	Trp	Lys	Tyr	Ser	His	Arg	Asn	His
	130					135					140				
His	Ala	Asn	Thr	Ser	Ser	Ile	Asp	Asn	Asp	Glu	Val	Tyr	Ile	Pro	Lys
145					150					155					160
Ser	Lys	Ser	Lys	Leu	Ala	Leu	Thr	Tyr	Lys	Leu	Leu	Asn	Asn	Pro	Pro
			165						170					175	
Gly	Arg	Leu	Leu	Val	Met	Val	Ile	Met	Phe	Thr	Leu	Gly	Phe	Pro	Leu
			180					185					190		
Tyr	Leu	Leu	Thr	Asn	Ile	Ser	Gly	Lys	Lys	Tyr	Asp	Arg	Phe	Ala	Asn
	195						200					205			
His	Phe	Asp	Pro	Met	Ser	Pro	Ile	Phe	Lys	Glu	Arg	Glu	Arg	Phe	Gln
	210					215					220				
Val	Leu	Leu	Ser	Asp	Leu	Gly	Leu	Leu	Ala	Val	Phe	Tyr	Gly	Ile	Lys
225					230					235					240
Val	Ala	Val	Ala	Lys	Lys	Gly	Ala	Ala	Trp	Val	Ala	Cys	Met	Tyr	Gly
			245						250					255	
Val	Pro	Met	Leu	Gly	Val	Phe	Thr	Leu	Phe	Asp	Ile	Ile	Thr	Tyr	Leu
			260					265					270		
His	His	Thr	His	Gln	Ser	Ser	Pro	His	Tyr	Asp	Ser	Thr	Glu	Trp	Asn
	275						280					285			
Trp	Ile	Arg	Gly	Ala	Leu	Ser	Ala	Ile	Asp	Arg	Asp	Phe	Gly	Phe	Met
	290					295					300				
Asn	Ser	Val	Phe	His	Asp	Val	Thr	His	Thr	His	Val	Met	His	His	Met
305					310					315					320
Phe	Ser	Tyr	Ile	Pro	His	Tyr	His	Ala	Lys	Glu	Ala	Arg	Asp	Ala	Ile
			325						330					335	
Asn	Thr	Ile	Ile	Gly	Asp	Tyr	Tyr	Met	Ile	Asp	Arg	Thr	Pro	Ile	Leu
			340					345					350		
Lys	Ala	Leu	Trp	Arg	Glu	Ala	Lys	Glu	Cys	Met	Tyr	Ile	Glu	Pro	Asp
	355						360					365			
Ser	Lys	Arg	Lys	Gly	Val	Tyr	Trp	Tyr	His	Lys	Leu				
	370					375					380				

&lt;210&gt; 25

&lt;211&gt; 1152

&lt;212&gt; DNA

&lt;213&gt; Ricinus communis

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(1149)

&lt;400&gt; 25

atg	gga	ggt	ggt	ggt	cgc	atg	tct	act	gtc	ata	acc	agc	aac	aac	agt	48
Met	Gly	Gly	Gly	Gly	Arg	Met	Ser	Thr	Val	Ile	Thr	Ser	Asn	Asn	Ser	
1				5					10					15		

gag	agc	agc	cac	ctt	aag	cga	gcg	ccg	cac	acg	aag	cct	cct	ttc	aca	96
Glu	Ser	Ser	His	Leu	Lys	Arg	Ala	Pro	His	Thr	Lys	Pro	Pro	Phe	Thr	
			20					25						30		

ctt ggt gac ctc aag aga gcc atc cca ccc cat tgc ttt gaa cgc tct	144
Leu Gly Asp Leu Lys Arg Ala Ile Pro Pro His Cys Phe Glu Arg Ser	
35 40 45	
ttt gtg cgc tca ttc tcc tat gtt gcc tat gat gtc tgc tta agt ttt	192
Phe Val Arg Ser Phe Ser Tyr Val Ala Tyr Asp Val Cys Leu Ser Phe	
50 55 60	
ctt ttc tac tcg atc gcc acc aac ttc ttc cct tac atc tct tct ccg	240
Leu Phe Tyr Ser Ile Ala Thr Asn Phe Phe Pro Tyr Ile Ser Ser Pro	
65 70 75 80	
ctc tcg tat gtc gct tgg ctg gtt tac tgg ctc ttc caa ggc tgc att	288
Leu Ser Tyr Val Ala Trp Leu Val Tyr Trp Leu Phe Gln Gly Cys Ile	
85 90 95	
ctc act ggt ctt tgg gtc atc ggc cat gaa tgt ggc cat cat gct ttt	336
Leu Thr Gly Leu Trp Val Ile Gly His Glu Cys Gly His His Ala Phe	
100 105 110	
agt gag tat cag ctg gct gat gac att gtt ggc cta att gtc cat tct	384
Ser Glu Tyr Gln Leu Ala Asp Asp Ile Val Gly Leu Ile Val His Ser	
115 120 125	
gca ctt ctg gtt cca tat ttt tca tgg aaa tat agc cat cgc cgc cac	432
Ala Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg His	
130 135 140	
cat tct aac ata gga tct ctc gag cga gac gaa gtg ttc gtc ccg aaa	480
His Ser Asn Ile Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys	
145 150 155 160	
tca aag tcg aaa att tca tgg tat tct aag tac tta aac aac ccg cca	528
Ser Lys Ser Lys Ile Ser Trp Tyr Ser Lys Tyr Leu Asn Asn Pro Pro	
165 170 175	
ggt cga gtt ttg aca ctt gct gcc acg ctc ctc ctt ggc tgg cct tta	576
Gly Arg Val Leu Thr Leu Ala Ala Thr Leu Leu Leu Gly Trp Pro Leu	
180 185 190	
tac tta gct ttc aat gtc tct ggt aga cct tac gat cgc ttt gct tgc	624
Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Arg Phe Ala Cys	
195 200 205	
cat tat gat ccc tat ggc cca ata ttt tcc gaa aga gaa agg ctt cag	672
His Tyr Asp Pro Tyr Gly Pro Ile Phe Ser Glu Arg Glu Arg Leu Gln	
210 215 220	
att tac att gct gac ctc gga atc ttt gcc aca acg ttt gtg ctt tat	720
Ile Tyr Ile Ala Asp Leu Gly Ile Phe Ala Thr Thr Phe Val Leu Tyr	
225 230 235 240	
cag gct aca atg gca aaa ggg ttg gct tgg gta atg cgt atc tat ggg	768
Gln Ala Thr Met Ala Lys Gly Leu Ala Trp Val Met Arg Ile Tyr Gly	
245 250 255	

gtg cca ttg ctt att gtt aac tgt ttc ctt gtt atg atc aca tac ttg 816  
 Val Pro Leu Leu Ile Val Asn Cys Phe Leu Val Met Ile Thr Tyr Leu  
 260 265 270

cag cac act cac cca gct att cca cgc tat ggc tca tcg gaa tgg gat 864  
 Gln His Thr His Pro Ala Ile Pro Arg Tyr Gly Ser Ser Glu Trp Asp  
 275 280 285

tgg ctc cgg gga gca atg gtg act gtc gat aga gat tat ggg gtg ttg 912  
 Trp Leu Arg Gly Ala Met Val Thr Val Asp Arg Asp Tyr Gly Val Leu  
 290 295 300

aat aaa gta ttc cat aac att gca gac act cat gta gct cat cat ctc 960  
 Asn Lys Val Phe His Asn Ile Ala Asp Thr His Val Ala His His Leu  
 305 310 315 320

ttt gct aca gtg cca cat tac cat gca atg gag gcc act aaa gca atc 1008  
 Phe Ala Thr Val Pro His Tyr His Ala Met Glu Ala Thr Lys Ala Ile  
 325 330 335

aag cct ata atg ggt gag tat tac cgg tat gat ggt acc cca ttt tac 1056  
 Lys Pro Ile Met Gly Glu Tyr Tyr Arg Tyr Asp Gly Thr Pro Phe Tyr  
 340 345 350

aag gca ttg tgg agg gag gca aag gag tgc ttg ttc gtc gag cca gat 1104  
 Lys Ala Leu Trp Arg Glu Ala Lys Glu Cys Leu Phe Val Glu Pro Asp  
 355 360 365

gaa gga gct cct aca caa ggc gtt ttc tgg tac cgg aac aag tat 1149  
 Glu Gly Ala Pro Thr Gln Gly Val Phe Trp Tyr Arg Asn Lys Tyr  
 370 375 380

taa 1152

<210> 26  
 <211> 1152  
 <212> DNA  
 <213> *Lesquerella gracilis* B

<220>  
 <221> CDS  
 <222> (1)...(1149)

<400> 26

atg ggt gct ggt gga aga ata atg gtt acc cct tct tcc aag aaa tca 48  
 Met Gly Ala Gly Gly Arg Ile Met Val Thr Pro Ser Ser Lys Lys Ser  
 1 5 10 15

gaa act gaa gcc cta aaa cgt gga cca tgt gag aaa cca cca ttc act 96  
 Glu Thr Glu Ala Leu Lys Arg Gly Pro Cys Glu Lys Pro Pro Phe Thr  
 20 25 30

gtt aaa gat ctg aag aaa gca atc cca cag cat tgt ttt caa cgc tct 144  
 Val Lys Asp Leu Lys Lys Ala Ile Pro Gln His Cys Phe Gln Arg Ser  
 35 40 45

atc cct cgt tct ttc tcc tac ctt ctc aca gat atc act tta gtt tct 192

Ile	Pro	Arg	Ser	Phe	Ser	Tyr	Leu	Leu	Thr	Asp	Ile	Thr	Leu	Val	Ser		
	50					55					60						
tgc	ttc	tac	tac	gtt	gcc	aca	aat	tac	ttc	tct	ctt	ctt	cct	cag	cct		240
Cys	Phe	Tyr	Tyr	Val	Ala	Thr	Asn	Tyr	Phe	Ser	Leu	Leu	Pro	Gln	Pro		
	65				70				75						80		
ctc	tct	tac	cta	gct	tgg	cct	ctc	tat	tgg	gta	tgt	caa	ggc	tgt	gtc		288
Leu	Ser	Tyr	Leu	Ala	Trp	Pro	Leu	Tyr	Trp	Val	Cys	Gln	Gly	Cys	Val		
				85					90					95			
cta	aca	ggg	atc	tgg	gtc	ctt	ggc	cat	gaa	tgt	ggg	cac	cat	gca	ttc		336
Leu	Thr	Gly	Ile	Trp	Val	Leu	Gly	His	Glu	Cys	Gly	His	His	Ala	Phe		
			100					105						110			
agt	gac	tat	caa	tgg	cta	gat	gac	act	gtt	ggg	ttt	atc	ttc	cat	tcc		384
Ser	Asp	Tyr	Gln	Trp	Leu	Asp	Asp	Thr	Val	Gly	Phe	Ile	Phe	His	Ser		
		115					120					125					
tta	ctt	ctc	gtc	cct	tac	ttc	tcc	tgg	aaa	tac	agt	cat	cgf	cgf	cac		432
Leu	Leu	Leu	Val	Pro	Tyr	Phe	Ser	Trp	Lys	Tyr	Ser	His	Arg	Arg	His		
	130					135					140						
cat	tcc	aac	aat	gga	tct	ctc	gag	aaa	gat	gaa	gtc	ttt	gtc	cca	ccg		480
His	Ser	Asn	Asn	Gly	Ser	Leu	Glu	Lys	Asp	Glu	Val	Phe	Val	Pro	Pro		
	145				150				155					160			
aaa	aaa	gct	gca	gtc	aaa	tgg	tat	gtt	aaa	tac	ctc	aac	aac	cct	ctt		528
Lys	Lys	Ala	Ala	Val	Lys	Trp	Tyr	Val	Lys	Tyr	Leu	Asn	Asn	Pro	Leu		
				165					170					175			
gga	cgf	att	ctg	gtg	tta	aca	gtt	cgf	ttt	atc	ctc	ggg	tgg	cct	ttg		576
Gly	Arg	Ile	Leu	Val	Leu	Thr	Val	Arg	Phe	Ile	Leu	Gly	Trp	Pro	Leu		
			180					185					190				
tat	cta	gcc	ttt	aat	gta	tca	ggg	aga	cct	tat	gat	ggg	ttc	gct	tca		624
Tyr	Leu	Ala	Phe	Asn	Val	Ser	Gly	Arg	Pro	Tyr	Asp	Gly	Phe	Ala	Ser		
		195					200					205					
cat	ttc	ttc	cct	cat	gca	cct	atc	ttt	aaa	gac	cgf	gaa	cgf	ctc	cag		672
His	Phe	Phe	Pro	His	Ala	Pro	Ile	Phe	Lys	Asp	Arg	Glu	Arg	Leu	Gln		
	210					215					220						
ata	tac	atc	tca	gat	gct	ggg	att	cta	gct	gtc	tgt	tat	ggg	ctt	tac		720
Ile	Tyr	Ile	Ser	Asp	Ala	Gly	Ile	Leu	Ala	Val	Cys	Tyr	Gly	Leu	Tyr		
	225				230					235				240			
cgf	tac	gct	gct	tca	caa	gga	ttg	acc	gct	atg	atc	tgc	gtc	tat	gga		768
Arg	Tyr	Ala	Ala	Ser	Gln	Gly	Leu	Thr	Ala	Met	Ile	Cys	Val	Tyr	Gly		
				245					250					255			
gta	ccg	ctt	ttg	ata	gtg	aac	ttt	ttc	ctt	gtc	ttg	gta	act	ttc	ttg		816
Val	Pro	Leu	Leu	Ile	Val	Asn	Phe	Phe	Leu	Val	Leu	Val	Thr	Phe	Leu		
			260					265					270				
cag	cac	act	cat	cct	tcg	tta	cct	cac	tat	gat	tca	acc	gag	tgg	gaa		864
Gln	His	Thr	His	Pro	Ser	Leu	Pro	His	Tyr	Asp	Ser	Thr	Glu	Trp	Glu		

275	280	285	
tgg att aga gga gct ttg gtt acg gta gac aga gac tac gga atc ttg			912
Trp Ile Arg Gly Ala Leu Val Thr Val Asp Arg Asp Tyr Gly Ile Leu			
290	295	300	
aac aag gtg ttt cac aac ata aca gac aca cat gtg gct cat cat ctt			960
Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His Leu			
305	310	315	320
ttc gca act ata ccg cat tat aac gca atg gaa gct aca gag gcg ata			1008
Phe Ala Thr Ile Pro His Tyr Asn Ala Met Glu Ala Thr Glu Ala Ile			
	325	330	335
aag cca ata ctt ggt gat tac tac cat ttc gat gga aca ccg tgg tat			1056
Lys Pro Ile Leu Gly Asp Tyr Tyr His Phe Asp Gly Thr Pro Trp Tyr			
	340	345	350
gtg gct atg tat agg gaa gca aag gag tgt ctc tat gta gaa ccg gat			1104
Val Ala Met Tyr Arg Glu Ala Lys Glu Cys Leu Tyr Val Glu Pro Asp			
	355	360	365
acg gaa cgt ggg aag aaa ggt gtc tac tat tac aac aat aag tta			1149
Thr Glu Arg Gly Lys Lys Gly Val Tyr Tyr Tyr Asn Asn Lys Leu			
	370	375	380
tga			1152
<210> 27			
<211> 1134			
<212> DNA			
<213> Stokesia laevis			
<220>			
<221> CDS			
<222> (1)...(1131)			
<400> 27			
atg ggt gca ggt ggt cgg atg tcg gat cta tct gac gga aaa aat ctc			48
Met Gly Ala Gly Gly Arg Met Ser Asp Leu Ser Asp Gly Lys Asn Leu			
1	5	10	15
ctc aaa cgt gtg cca gtt gat cca cct ttc aca tta agt gat ata aag			96
Leu Lys Arg Val Pro Val Asp Pro Pro Phe Thr Leu Ser Asp Ile Lys			
	20	25	30
aaa gca atc cct ccc cat tgc ttc aaa cga tct gtc ata cgt tcg tcc			144
Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser Val Ile Arg Ser Ser			
	35	40	45
tac tat gtt gtt cat gat ctc atc gtc tcc tac gtc ttc ttc ttc ctc			192
Tyr Tyr Val Val His Asp Leu Ile Val Ser Tyr Val Phe Phe Phe Leu			
	50	55	60
gca acg aca tat att act gtt ctt cct gct cct ctt gct tac ata gcg			240
Ala Thr Thr Tyr Ile Thr Val Leu Pro Ala Pro Leu Ala Tyr Ile Ala			
	65	70	75
			80

tgg cca gtt tac tgg ttt tgc caa gca agt att ctc act ggg ttg tgg	288
Trp Pro Val Tyr Trp Phe Cys Gln Ala Ser Ile Leu Thr Gly Leu Trp	
85 90 95	
gtt atc ggc cat gaa tgt ggt cac cat gcc ttt agt gaa tac cag tgg	336
Val Ile Gly His Glu Cys Gly His His Ala Phe Ser Glu Tyr Gln Trp	
100 105 110	
att gat gac aca gtt ggg ttc atc ctc cac tcg gct ctc ctc acc cct	384
Ile Asp Asp Thr Val Gly Phe Ile Leu His Ser Ala Leu Leu Thr Pro	
115 120 125	
tac ttc tct tgg aaa tat agc cat cga aat cac cat gcg aac aca aat	432
Tyr Phe Ser Trp Lys Tyr Ser His Arg Asn His His Ala Asn Thr Asn	
130 135 140	
tca ctc gac aac gac gaa gtt tac att cct aag cgc aag tcc aaa gtc	480
Ser Leu Asp Asn Asp Glu Val Tyr Ile Pro Lys Arg Lys Ser Lys Val	
145 150 155 160	
aag att tac tcc aaa atc cta aac aac cca cct gga cga gtg ttc act	528
Lys Ile Tyr Ser Lys Ile Leu Asn Asn Pro Pro Gly Arg Val Phe Thr	
165 170 175	
ttg gtt ttc agg ttg acg cta ggg ttt cct ttg tac ctg tta act aat	576
Leu Val Phe Arg Leu Thr Leu Gly Phe Pro Leu Tyr Leu Leu Thr Asn	
180 185 190	
atc tct gga aag aaa tac caa cgg ttt gcc aac cac ttt gat cca ttg	624
Ile Ser Gly Lys Lys Tyr Gln Arg Phe Ala Asn His Phe Asp Pro Leu	
195 200 205	
agt ccc atc ttc acc gag cgt gaa cga att cag gtt ctt gta tca gat	672
Ser Pro Ile Phe Thr Glu Arg Glu Arg Ile Gln Val Leu Val Ser Asp	
210 215 220	
ctt ggt ctt cta gct gta atc tac gca atc aag ctt ctt gtt gct gca	720
Leu Gly Leu Leu Ala Val Ile Tyr Ala Ile Lys Leu Leu Val Ala Ala	
225 230 235 240	
aaa gga gct gtc tgg gtg aca tgc atc tat gga gtt cca gtc cta ggt	768
Lys Gly Ala Val Trp Val Thr Cys Ile Tyr Gly Val Pro Val Leu Gly	
245 250 255	
gta agc gtg ttc ttc gtt ttg atc acg tat tta cac cac acc cat ctc	816
Val Ser Val Phe Phe Val Leu Ile Thr Tyr Leu His His Thr His Leu	
260 265 270	
tcc tta cct cat tac gat tcg act gag tgg aac tgg atc aga ggg gca	864
Ser Leu Pro His Tyr Asp Ser Thr Glu Trp Asn Trp Ile Arg Gly Ala	
275 280 285	
ttg tca acc atc gat agg gat ttt ggg ttc cta aat agg gtt ttc cat	912
Leu Ser Thr Ile Asp Arg Asp Phe Gly Phe Leu Asn Arg Val Phe His	
290 295 300	



gac gtt aca cac act cat gta ttg cat cat ttg atc tct tac att cca 960  
 Asp Val Thr His Thr His Val Leu His His Leu Ile Ser Tyr Ile Pro  
 305 310 315 320

cac tat cat gca aag gag gca aga gat gca atc aaa cca gtt ttg ggt 1008  
 His Tyr His Ala Lys Glu Ala Arg Asp Ala Ile Lys Pro Val Leu Gly  
 325 330 335

gat tat tat aag att gat agg act ccg ata ttc aaa gca atg tgg aga 1056  
 Asp Tyr Tyr Lys Ile Asp Arg Thr Pro Ile Phe Lys Ala Met Trp Arg  
 340 345 350

gag gcc aag gaa tgc atc tat atc gag cca gat gaa gat act gaa cac 1104  
 Glu Ala Lys Glu Cys Ile Tyr Ile Glu Pro Asp Glu Asp Thr Glu His  
 355 360 365

aag ggt gtt tac tgg tac cat aaa atg tga 1134  
 Lys Gly Val Tyr Trp Tyr His Lys Met  
 370 375

<210> 28  
 <211> 1164  
 <212> DNA  
 <213> Ricinus communis

<220>  
 <221> CDS  
 <222> (1)...(1161)

<400> 28

atg gct tcc tcc gga aga atg tct act gtg att act tct aac aac tct 48  
 Met Ala Ser Ser Gly Arg Met Ser Thr Val Ile Thr Ser Asn Asn Ser  
 1 5 10 15

gag aag aag gga ggt tct tct cat ctt aag aga gct cca cat act aag 96  
 Glu Lys Lys Gly Gly Ser Ser His Leu Lys Arg Ala Pro His Thr Lys  
 20 25 30

cca cct ttc act ctt gga gac ctt aag aga gct att cca cct cat tgt 144  
 Pro Pro Phe Thr Leu Gly Asp Leu Lys Arg Ala Ile Pro Pro His Cys  
 35 40 45

ttc gag aga tct ttc gtg aga tct ttc tct tat gtg gct tat gac gtg 192  
 Phe Glu Arg Ser Phe Val Arg Ser Phe Ser Tyr Val Ala Tyr Asp Val  
 50 55 60

tgt ctt tct ttc ctt ttc tat tct att gct act aac ttc ttc cca tat 240  
 Cys Leu Ser Phe Leu Phe Tyr Ser Ile Ala Thr Asn Phe Phe Pro Tyr  
 65 70 75 80

att tct tct cca ctt tct tat gtg gct tgg ctt gtg tat tgg ctt ttc 288  
 Ile Ser Ser Pro Leu Ser Tyr Val Ala Trp Leu Val Tyr Trp Leu Phe  
 85 90 95

caa gga tgt att ctt act gga ctt tgg gtt att ggt cat gag tgt ggt 336  
 Gln Gly Cys Ile Leu Thr Gly Leu Trp Val Ile Gly His Glu Cys Gly  
 100 105 110

cat cat gca ttt tct gaa tat caa ctt gct gac gac att gtg gga ctt	384
His His Ala Phe Ser Glu Tyr Gln Leu Ala Asp Asp Ile Val Gly Leu	
115 120 125	
att gtg cat tct gct ctt ttg gtg cca tat ttc tct tgg aag tat tct	432
Ile Val His Ser Ala Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser	
130 135 140	
cat aga aga cat cat tct aac att gga tct ctt gag aga gac gag gtg	480
His Arg Arg His His Ser Asn Ile Gly Ser Leu Glu Arg Asp Glu Val	
145 150 155 160	
ttt gtg cct aag tct aag tct aag att tct tgg tat tct aag tat ctt	528
Phe Val Pro Lys Ser Lys Ser Lys Ile Ser Trp Tyr Ser Lys Tyr Leu	
165 170 175	
aac aac cca cct gga aga gtg ctt act ctt gct gca act ctt ttg ctt	576
Asn Asn Pro Pro Gly Arg Val Leu Thr Leu Ala Ala Thr Leu Leu Leu	
180 185 190	
gga tgg cca ctt tat ctt gct ttc aac gtg tct gga aga cca tat gac	624
Gly Trp Pro Leu Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp	
195 200 205	
aga ttc gct tgt cat tat gac cca tat gga cca att ttc tct gag aga	672
Arg Phe Ala Cys His Tyr Asp Pro Tyr Gly Pro Ile Phe Ser Glu Arg	
210 215 220	
gag aga ctt caa atc tat att gct gac ctt gga att ttc gct act act	720
Glu Arg Leu Gln Ile Tyr Ile Ala Asp Leu Gly Ile Phe Ala Thr Thr	
225 230 235 240	
ttc gtg ctt tat caa gct act atg gct aag gga ctt gct tgg gtt atg	768
Phe Val Leu Tyr Gln Ala Thr Met Ala Lys Gly Leu Ala Trp Val Met	
245 250 255	
aga atc tat gga gtg cca ctt ttg att gtg aac tgt ttc ctt gtg atg	816
Arg Ile Tyr Gly Val Pro Leu Leu Ile Val Asn Cys Phe Leu Val Met	
260 265 270	
att act tat ctt caa cat act cat cca gct att cca aga tat gga tct	864
Ile Thr Tyr Leu Gln His Thr His Pro Ala Ile Pro Arg Tyr Gly Ser	
275 280 285	
tct gaa tgg gat tgg ctt aga gga gct atg gtg act gtg gac aga gac	912
Ser Glu Trp Asp Trp Leu Arg Gly Ala Met Val Thr Val Asp Arg Asp	
290 295 300	
tat gga gtg ctt aac aag gtg ttc cat aac att gct gac act cat gtg	960
Tyr Gly Val Leu Asn Lys Val Phe His Asn Ile Ala Asp Thr His Val	
305 310 315 320	
gct cat cat ctt ttc gct act gtg cca cat tat cat gct atg gag gct	1008
Ala His His Leu Phe Ala Thr Val Pro His Tyr His Ala Met Glu Ala	
325 330 335	

act aag gct att aag cca att atg gga gag tat tat aga tat gac gga 1056  
 Thr Lys Ala Ile Lys Pro Ile Met Gly Glu Tyr Tyr Arg Tyr Asp Gly  
 340 345 350

act cca ttc tat aag gct ctt tgg aga gag gct aag gag tgt ctt ttc 1104  
 Thr Pro Phe Tyr Lys Ala Leu Trp Arg Glu Ala Lys Glu Cys Leu Phe  
 355 360 365

gtt gaa cca gat gaa gga gct cca act caa gga gtg ttc tgg tat aga 1152  
 Val Glu Pro Asp Glu Gly Ala Pro Thr Gln Gly Val Phe Trp Tyr Arg  
 370 375 380

aac aag tat taa 1164  
 Asn Lys Tyr  
 385

<210> 29  
 <211> 1134  
 <212> DNA  
 <213> Stokesia laevis

<220>  
 <221> CDS  
 <222> (1)...(1131)

<400> 29

atg gct tcc tcc gga aga atg tct gac ctt tct gac gga aag aac ctt 48  
 Met Ala Ser Ser Gly Arg Met Ser Asp Leu Ser Asp Gly Lys Asn Leu  
 1 5 10 15

ttg aag aga gtg cca gtg gac cca cct ttc act ctt tct gac att aag 96  
 Leu Lys Arg Val Pro Val Asp Pro Pro Phe Thr Leu Ser Asp Ile Lys  
 20 25 30

aag gct att cca cct cat tgt ttc aag aga tct gtg att aga tct tct 144  
 Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser Val Ile Arg Ser Ser  
 35 40 45

tat tat gtg gtg cat gac ctt att gtg tct tat gtg ttc ttc ttc ctt 192  
 Tyr Tyr Val Val His Asp Leu Ile Val Ser Tyr Val Phe Phe Phe Leu  
 50 55 60

gct act act tat att act gtg ctt cca gct cca ctt gct tat att gct 240  
 Ala Thr Thr Tyr Ile Thr Val Leu Pro Ala Pro Leu Ala Tyr Ile Ala  
 65 70 75 80

tgg cca gtg tat tgg ttc tgt caa gct tct att ctt act gga ctt tgg 288  
 Trp Pro Val Tyr Trp Phe Cys Gln Ala Ser Ile Leu Thr Gly Leu Trp  
 85 90 95

gtt att gga cat gag tgt gga cat cat gct ttc tct gag tat caa tgg 336  
 Val Ile Gly His Glu Cys Gly His His Ala Phe Ser Glu Tyr Gln Trp  
 100 105 110

att gac gac act gtg gga ttc att ctt cat tct gct ctt ttg act cca 384  
 Ile Asp Asp Thr Val Gly Phe Ile Leu His Ser Ala Leu Leu Thr Pro  
 115 120 125

tat ttc tct tgg aag tat tct cat aga aac cat cat gct aac act aac	432
Tyr Phe Ser Trp Lys Tyr Ser His Arg Asn His His Ala Asn Thr Asn	
130 135 140	
tct ctt gac aac gac gag gtg tat att cca aag aga aag tct aag gtg	480
Ser Leu Asp Asn Asp Glu Val Tyr Ile Pro Lys Arg Lys Ser Lys Val	
145 150 155 160	
aag atc tat tct aag att ctt aac aac cca cct gga aga gtg ttc act	528
Lys Ile Tyr Ser Lys Ile Leu Asn Asn Pro Pro Gly Arg Val Phe Thr	
165 170 175	
ctt gtg ttc aga ctt act ctt gga ttc cca ctt tat ctt ttg act aac	576
Leu Val Phe Arg Leu Thr Leu Gly Phe Pro Leu Tyr Leu Leu Thr Asn	
180 185 190	
att tct gga aag aag tat caa aga ttc gct aac cat ttc gac cca ctt	624
Ile Ser Gly Lys Lys Tyr Gln Arg Phe Ala Asn His Phe Asp Pro Leu	
195 200 205	
tct cca att ttc act gag aga gag aga att caa gtg ctt gtg tct gac	672
Ser Pro Ile Phe Thr Glu Arg Glu Arg Ile Gln Val Leu Val Ser Asp	
210 215 220	
ctt gga ctt ttg gct gtg atc tat gct att aag ctt ttg gtt gct gca	720
Leu Gly Leu Leu Ala Val Ile Tyr Ala Ile Lys Leu Leu Val Ala Ala	
225 230 235 240	
aag gga gct gtg tgg gtg act tgt atc tat gga gtt cca gtt ctt gga	768
Lys Gly Ala Val Trp Val Thr Cys Ile Tyr Gly Val Pro Val Leu Gly	
245 250 255	
gtg tct gtg ttc ttc gtg ctt att act tat ctt cat cat act cat ctt	816
Val Ser Val Phe Phe Val Leu Ile Thr Tyr Leu His His Thr His Leu	
260 265 270	
tct ctt cca cat tat gac tct act gag tgg aac tgg att aga gga gct	864
Ser Leu Pro His Tyr Asp Ser Thr Glu Trp Asn Trp Ile Arg Gly Ala	
275 280 285	
ctt tct act att gac aga gac ttc gga ttc ctt aac aga gtg ttc cat	912
Leu Ser Thr Ile Asp Arg Asp Phe Gly Phe Leu Asn Arg Val Phe His	
290 295 300	
gac gtg act cat act cat gtg ctt cat cat ctt att tct tat att cca	960
Asp Val Thr His Thr His Val Leu His His Leu Ile Ser Tyr Ile Pro	
305 310 315 320	
cat tat cat gct aag gag gct aga gac gct att aag cca gtg ctt gga	1008
His Tyr His Ala Lys Glu Ala Arg Asp Ala Ile Lys Pro Val Leu Gly	
325 330 335	
gac tat tat aag att gac aga act cca atc ttt aag gct atg tgg aga	1056
Asp Tyr Tyr Lys Ile Asp Arg Thr Pro Ile Phe Lys Ala Met Trp Arg	
340 345 350	

gag gct aag gag tgt atc tat att gaa cca gac gaa gac act gag cat 1104  
 Glu Ala Lys Glu Cys Ile Tyr Ile Glu Pro Asp Glu Asp Thr Glu His  
 355 360 365

aag gga gtg tat tgg tat cat aag atg taa 1134  
 Lys Gly Val Tyr Trp Tyr His Lys Met  
 370 375

<210> 30  
 <211> 1164  
 <212> DNA  
 <213> Ricinus communis

<220>  
 <221> CDS  
 <222> (1)...(1161)

<400> 30

atg gct tcc tcc ggt agg atg tct act gtc ata acc agc aac aac agt 48  
 Met Ala Ser Ser Gly Arg Met Ser Thr Val Ile Thr Ser Asn Asn Ser  
 1 5 10 15

gag aag aaa gga gga agc agt cac ctt aag agg gct cca cac act aag 96  
 Glu Lys Lys Gly Gly Ser Ser His Leu Lys Arg Ala Pro His Thr Lys  
 20 25 30

cct cct ttc aca ctt ggt gac ctc aag aga gcc atc cca ccc cat tgc 144  
 Pro Pro Phe Thr Leu Gly Asp Leu Lys Arg Ala Ile Pro Pro His Cys  
 35 40 45

ttt gaa agg tct ttt gtg aga tca ttc tcc tat gtt gcc tat gat gtc 192  
 Phe Glu Arg Ser Phe Val Arg Ser Phe Ser Tyr Val Ala Tyr Asp Val  
 50 55 60

tgc tta agt ttt ctt ttc tac tct atc gcc acc aac ttc ttc cct tac 240  
 Cys Leu Ser Phe Leu Phe Tyr Ser Ile Ala Thr Asn Phe Phe Pro Tyr  
 65 70 75 80

atc tct tct cca ctc tct tat gtc gct tgg ctg gtt tac tgg ctc ttc 288  
 Ile Ser Ser Pro Leu Ser Tyr Val Ala Trp Leu Val Tyr Trp Leu Phe  
 85 90 95

caa ggc tgc att ctc act ggt ctt tgg gtc atc ggc cat gaa tgt ggc 336  
 Gln Gly Cys Ile Leu Thr Gly Leu Trp Val Ile Gly His Glu Cys Gly  
 100 105 110

cat cat gct ttt agt gag tat cag ctg gct gat gac att gtt ggc cta 384  
 His His Ala Phe Ser Glu Tyr Gln Leu Ala Asp Asp Ile Val Gly Leu  
 115 120 125

att gtc cat tct gca ctt ctg gtt cca tac ttc tca tgg aaa tat agc 432  
 Ile Val His Ser Ala Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser  
 130 135 140

cat aga agg cac cat tct aac ata gga tct ctc gag agg gac gaa gtg 480  
 His Arg Arg His His Ser Asn Ile Gly Ser Leu Glu Arg Asp Glu Val  
 145 150 155 160

ttc gtc cca aaa tca aag tct aaa att tca tgg tat tct aag tac tta	528
Phe Val Pro Lys Ser Lys Ser Lys Ile Ser Trp Tyr Ser Lys Tyr Leu	
165 170 175	
aac aac cct cca ggt agg gtt ttg aca ctt gct gcc act ctt ctc ctt	576
Asn Asn Pro Pro Gly Arg Val Leu Thr Leu Ala Ala Thr Leu Leu Leu	
180 185 190	
ggc tgg cct tta tac tta gct ttc aat gtc tct ggt aga cct tac gat	624
Gly Trp Pro Leu Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp	
195 200 205	
agg ttt gct tgc cat tat gat ccc tat ggc cca ata ttt tcc gaa aga	672
Arg Phe Ala Cys His Tyr Asp Pro Tyr Gly Pro Ile Phe Ser Glu Arg	
210 215 220	
gaa agg ctt cag atc tac att gct gac ctc gga atc ttt gcc aca act	720
Glu Arg Leu Gln Ile Tyr Ile Ala Asp Leu Gly Ile Phe Ala Thr Thr	
225 230 235 240	
ttt gtg ctt tat cag gct aca atg gca aaa ggg ttg gct tgg gta atg	768
Phe Val Leu Tyr Gln Ala Thr Met Ala Lys Gly Leu Ala Trp Val Met	
245 250 255	
agg atc tat ggg gtg cca ttg ctt att gtt aac tgt ttc ctt gtt atg	816
Arg Ile Tyr Gly Val Pro Leu Leu Ile Val Asn Cys Phe Leu Val Met	
260 265 270	
atc aca tac ttg cag cac act cac cca gct att cca agg tat ggc tca	864
Ile Thr Tyr Leu Gln His Thr His Pro Ala Ile Pro Arg Tyr Gly Ser	
275 280 285	
tct gaa tgg gat tgg ctc agg gga gca atg gtg act gtc gat aga gat	912
Ser Glu Trp Asp Trp Leu Arg Gly Ala Met Val Thr Val Asp Arg Asp	
290 295 300	
tat ggg gtg ttg aac aag gta ttc cat aac att gca gac act cat gta	960
Tyr Gly Val Leu Asn Lys Val Phe His Asn Ile Ala Asp Thr His Val	
305 310 315 320	
gct cat cat ctc ttt gct aca gtg cca cat tac cat gca atg gag gcc	1008
Ala His His Leu Phe Ala Thr Val Pro His Tyr His Ala Met Glu Ala	
325 330 335	
act aaa gca atc aag cct ata atg gga gag tat tac agg tat gat ggt	1056
Thr Lys Ala Ile Lys Pro Ile Met Gly Glu Tyr Tyr Arg Tyr Asp Gly	
340 345 350	
acc cca ttt tac aag gca ttg tgg agg gag gca aag gag tgc ttg ttc	1104
Thr Pro Phe Tyr Lys Ala Leu Trp Arg Glu Ala Lys Glu Cys Leu Phe	
355 360 365	
gtc gag cca gat gaa gga gct cct aca caa ggc gtt ttc tgg tac agg	1152
Val Glu Pro Asp Glu Gly Ala Pro Thr Gln Gly Val Phe Trp Tyr Arg	
370 375 380	

```

aac aag tat taa                                     1164
Asn Lys Tyr
385

<210> 31
<211> 1155
<212> DNA
<213> Artificial Sequence

<220>
<223> hypothetical sequence

<221> CDS
<222> (1)...(1152)

<400> 31
atg gct tcc tcc gga aga atc atg gtt act cct tct tcc aag aag tca      48
Met Ala Ser Ser Gly Arg Ile Met Val Thr Pro Ser Ser Lys Lys Ser
  1             5             10             15

gaa act gaa gcc cta aag cgt gga cca tgt gag aaa cca cca ttc act      96
Glu Thr Glu Ala Leu Lys Arg Gly Pro Cys Glu Lys Pro Pro Phe Thr
             20             25             30

gtt aaa gat ctg aag aag gca atc cca cag cat tgt ttc caa aga tct     144
Val Lys Asp Leu Lys Lys Ala Ile Pro Gln His Cys Phe Gln Arg Ser
             35             40             45

atc cct cgt tct ttc tcc tac ctt ctc aca gat atc act tta gtt tct     192
Ile Pro Arg Ser Phe Ser Tyr Leu Leu Thr Asp Ile Thr Leu Val Ser
             50             55             60

tgc ttc tac tac gtt gcc aca aat tac ttc tct ctt ctt cct cag cct     240
Cys Phe Tyr Tyr Val Ala Thr Asn Tyr Phe Ser Leu Leu Pro Gln Pro
             65             70             75             80

ctc tct act tac cta gct tgg cct ctc tat tgg gta tgt caa ggc tgt     288
Leu Ser Thr Tyr Leu Ala Trp Pro Leu Tyr Trp Val Cys Gln Gly Cys
             85             90             95

gtc cta aca ggt atc tgg gtc ctt ggc cat gaa tgt ggt cac cat gca     336
Val Leu Thr Gly Ile Trp Val Leu Gly His Glu Cys Gly His His Ala
             100            105            110

ttc agt gac tat caa tgg cta gat gac act gtt ggt ttc atc ttc cat     384
Phe Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Phe Ile Phe His
             115            120            125

tcc tta ctt ctc gtc cct tac ttc tcc tgg aaa tac agt cat cgt cgt     432
Ser Leu Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg
             130            135            140

cac cat tcc aac aat gga tct ctc gag aaa gat gaa gtc ttt gtc cca     480
His His Ser Asn Asn Gly Ser Leu Glu Lys Asp Glu Val Phe Val Pro
             145            150            155            160

cca aag aag gct gca gtc aaa tgg tat gtt aaa tac ctc aac aac cct     528

```

Pro Lys Lys Ala Ala Val Lys Trp Tyr Val Lys Tyr Leu Asn Asn Pro	
165	170 175
ctt gga agg att ctg gtg tta aca gtt agg ttt atc ctc ggg tgg cct	576
Leu Gly Arg Ile Leu Val Leu Thr Val Arg Phe Ile Leu Gly Trp Pro	
180	185 190
ttg tat cta gcc ttt aat gta tca ggt aga cct tat gat ggt ttc gct	624
Leu Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Phe Ala	
195	200 205
tca cat ttc ttc cct cat gca cct atc ttt aaa gac agg gaa cgt ctc	672
Ser His Phe Phe Pro His Ala Pro Ile Phe Lys Asp Arg Glu Arg Leu	
210	215 220
cag ata tac atc tca gat gct ggt att cta gct gtc tgt tat ggt ctt	720
Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu	
225	230 235 240
tac cgt tac gct gct tca caa gga ttg acc gct atg atc tgc gtc tat	768
Tyr Arg Tyr Ala Ala Ser Gln Gly Leu Thr Ala Met Ile Cys Val Tyr	
245	250 255
gga gta cct ctt ttg ata gtg aac ttc ttc ctt gtc ttg gta act ttc	816
Gly Val Pro Leu Leu Ile Val Asn Phe Phe Leu Val Leu Val Thr Phe	
260	265 270
ttg cag cac act cat cct tct tta cct cac tat gat tca acc gag tgg	864
Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Thr Glu Trp	
275	280 285
gaa tgg att aga gga gct ttg gtt act gta gac aga gac tac gga atc	912
Glu Trp Ile Arg Gly Ala Leu Val Thr Val Asp Arg Asp Tyr Gly Ile	
290	295 300
ttg aac aag gtg ttt cac aac ata aca gac aca cat gtg gct cat cat	960
Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His	
305	310 315 320
ttg ttc gca act ata cct cat tat aac gca atg gaa gct aca gag gct	1008
Leu Phe Ala Thr Ile Pro His Tyr Asn Ala Met Glu Ala Thr Glu Ala	
325	330 335
atc aag cca ata ctt ggt gat tac tac cat ttc gat gga aca cct tgg	1056
Ile Lys Pro Ile Leu Gly Asp Tyr Tyr His Phe Asp Gly Thr Pro Trp	
340	345 350
tat gtg gct atg tat agg gaa gca aag gag tgt ctc tat gta gaa cct	1104
Tyr Val Ala Met Tyr Arg Glu Ala Lys Glu Cys Leu Tyr Val Glu Pro	
355	360 365
gat act gaa cgt ggg aag aag ggt gtc tac tat tac aac aat aag tta	1152
Asp Thr Glu Arg Gly Lys Lys Gly Val Tyr Tyr Tyr Asn Asn Lys Leu	
370	375 380
taa	1155



<210> 32  
 <211> 1125  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> hypothetical sequence

<221> CDS  
 <222> (1)...(1122)

<400> 32  
 atg gct tcc tcc ggc cat agt cga aca tct aag aag tct gtc atg gaa 48  
 Met Ala Ser Ser Gly His Ser Arg Thr Ser Lys Lys Ser Val Met Glu  
 1 5 10 15

cgt gtc tct gtt gat cca gta ccc ttc tct cta agt gat ttg aag caa 96  
 Arg Val Ser Val Asp Pro Val Pro Phe Ser Leu Ser Asp Leu Lys Gln  
 20 25 30

gca atc cct ccc cat tgc ttc cag cga tct gtc atc cgt tca tct tac 144  
 Ala Ile Pro Pro His Cys Phe Gln Arg Ser Val Ile Arg Ser Ser Tyr  
 35 40 45

tat gta gtt cac gat ctc att att gcc tac atc ttc tac ttc ctt gcc 192  
 Tyr Val Val His Asp Leu Ile Ile Ala Tyr Ile Phe Tyr Phe Leu Ala  
 50 55 60

gac aaa tac att cca att ctc cct gct cct cta gcc tac tta gct tgg 240  
 Asp Lys Tyr Ile Pro Ile Leu Pro Ala Pro Leu Ala Tyr Leu Ala Trp  
 65 70 75 80

ccc ctt tac tgg ttc tgt caa gct agc atc ctc act ggt tta tgg atc 288  
 Pro Leu Tyr Trp Phe Cys Gln Ala Ser Ile Leu Thr Gly Leu Trp Ile  
 85 90 95

ctc ggt cat gaa tgc ggt cac cat gcc ttt agc gag tac caa tgg gtt 336  
 Leu Gly His Glu Cys Gly His His Ala Phe Ser Glu Tyr Gln Trp Val  
 100 105 110

gac gac act gtg ggc ttc atg gtc cac tca ttt ctt ctc act cct tac 384  
 Asp Asp Thr Val Gly Phe Met Val His Ser Phe Leu Leu Thr Pro Tyr  
 115 120 125

ttc tct tgg aaa tac agt cac agg aat cac cat gcc aac aca agt tcc 432  
 Phe Ser Trp Lys Tyr Ser His Arg Asn His His Ala Asn Thr Ser Ser  
 130 135 140

att gat aac gat gaa gtt tac att cct aag agc aag tcc aaa ctc gct 480  
 Ile Asp Asn Asp Glu Val Tyr Ile Pro Lys Ser Lys Ser Lys Leu Ala  
 145 150 155 160

ctt acc tat aag ctt ctt aac aac cct cca gga agg ctg tta gtt atg 528  
 Leu Thr Tyr Lys Leu Leu Asn Asn Pro Pro Gly Arg Leu Leu Val Met  
 165 170 175

gtt atc atg ttc acc cta gga ttt cct tta tac ctc ttg aca aat att 576

Val	Ile	Met	Phe	Thr	Leu	Gly	Phe	Pro	Leu	Tyr	Leu	Leu	Thr	Asn	Ile		
			180					185					190				
tcc	ggc	aag	aag	tac	gac	agg	ttt	gcc	aac	cac	ttc	gac	ccc	atg	agt		624
Ser	Gly	Lys	Lys	Tyr	Asp	Arg	Phe	Ala	Asn	His	Phe	Asp	Pro	Met	Ser		
		195					200					205					
cca	att	ttc	aag	gaa	cgt	gag	agg	ttt	cag	gtc	ttg	ctt	tct	gat	ctt		672
Pro	Ile	Phe	Lys	Glu	Arg	Glu	Arg	Phe	Gln	Val	Leu	Leu	Ser	Asp	Leu		
	210					215					220						
ggc	ctt	ctt	gct	gtg	ttt	tat	gga	atc	aaa	gtt	gct	gta	gca	aag	aag		720
Gly	Leu	Leu	Ala	Val	Phe	Tyr	Gly	Ile	Lys	Val	Ala	Val	Ala	Lys	Lys		
	225				230					235					240		
gga	gct	gct	tgg	gtg	gct	tgt	atg	tat	gga	gtt	cca	atg	cta	ggc	gta		768
Gly	Ala	Ala	Trp	Val	Ala	Cys	Met	Tyr	Gly	Val	Pro	Met	Leu	Gly	Val		
				245					250					255			
ttc	acc	ctt	ttc	gat	atc	atc	act	tac	ttg	cac	cac	acc	cat	cag	tca		816
Phe	Thr	Leu	Phe	Asp	Ile	Ile	Thr	Tyr	Leu	His	His	Thr	His	Gln	Ser		
			260					265					270				
tct	cct	cat	tat	gac	tca	act	gaa	tgg	aac	tgg	atc	aga	gga	gct	ttg		864
Ser	Pro	His	Tyr	Asp	Ser	Thr	Glu	Trp	Asn	Trp	Ile	Arg	Gly	Ala	Leu		
		275					280					285					
tca	gca	atc	gat	agg	gac	ttt	ggg	ttc	atg	aat	agt	gtc	ttc	cat	gat		912
Ser	Ala	Ile	Asp	Arg	Asp	Phe	Gly	Phe	Met	Asn	Ser	Val	Phe	His	Asp		
	290					295					300						
gtt	aca	cac	act	cac	gtc	atg	cat	cat	atg	ttc	tca	tac	att	cca	cac		960
Val	Thr	His	Thr	His	Val	Met	His	His	Met	Phe	Ser	Tyr	Ile	Pro	His		
	305				310					315					320		
tat	cat	gct	aag	gag	gca	agg	gat	gca	atc	aat	aca	atc	ata	ggc	gac		1008
Tyr	His	Ala	Lys	Glu	Ala	Arg	Asp	Ala	Ile	Asn	Thr	Ile	Ile	Gly	Asp		
				325				330						335			
tat	tat	atg	atc	gat	agg	act	cca	att	ttg	aaa	gca	ctg	tgg	aga	gag		1056
Tyr	Tyr	Met	Ile	Asp	Arg	Thr	Pro	Ile	Leu	Lys	Ala	Leu	Trp	Arg	Glu		
			340					345					350				
gcc	aag	gaa	tgc	atg	tac	atc	gag	cct	gat	agc	aag	agg	aag	ggt	gta		1104
Ala	Lys	Glu	Cys	Met	Tyr	Ile	Glu	Pro	Asp	Ser	Lys	Arg	Lys	Gly	Val		
		355					360					365					
tat	tgg	tac	cat	aaa	ttg	taa											1125
Tyr	Trp	Tyr	His	Lys	Leu												
	370																

&lt;210&gt; 33

&lt;211&gt; 1134

&lt;212&gt; DNA

&lt;213&gt; Stokesia laevis

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(1131)

&lt;400&gt; 33

atg gct tcc tcc ggt agg atg tct gat ctt tct gac ggt aag aat ctt	48
Met Ala Ser Ser Gly Arg Met Ser Asp Leu Ser Asp Gly Lys Asn Leu	
1 . 5 10 15	
ctc aaa agg gtg cca gtt gat cca cct ttc aca tta agt gat ata aag	96
Leu Lys Arg Val Pro Val Asp Pro Pro Phe Thr Leu Ser Asp Ile Lys	
20 25 30	
aaa gca atc cct ccc cat tgc ttc aaa agg tct gtc ata agg tct tca	144
Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser Val Ile Arg Ser Ser	
35 40 45	
tac tat gtt gtt cat gat ctc atc gtc tcc tac gtc ttc ttc ttc ctc	192
Tyr Tyr Val Val His Asp Leu Ile Val Ser Tyr Val Phe Phe Phe Leu	
50 55 60	
gca act aca tat att act gtt ctt cct gct cct ctt gct tac ata gct	240
Ala Thr Thr Tyr Ile Thr Val Leu Pro Ala Pro Leu Ala Tyr Ile Ala	
65 70 75 80	
tgg cca gtt tac tgg ttt tgc caa gca agt att ctc act ggg ttg tgg	288
Trp Pro Val Tyr Trp Phe Cys Gln Ala Ser Ile Leu Thr Gly Leu Trp	
85 90 95	
gtt atc ggc cat gaa tgt ggt cac cat gcc ttt agt gaa tac cag tgg	336
Val Ile Gly His Glu Cys Gly His His Ala Phe Ser Glu Tyr Gln Trp	
100 105 110	
att gat gac aca gtt ggg ttc atc ctc cac tct gct ctt ctc acc cct	384
Ile Asp Asp Thr Val Gly Phe Ile Leu His Ser Ala Leu Leu Thr Pro	
115 120 125	
tac ttc tct tgg aaa tat agc cat agg aat cac cat gct aac aca aat	432
Tyr Phe Ser Trp Lys Tyr Ser His Arg Asn His His Ala Asn Thr Asn	
130 135 140	
tca ctc gac aac gac gaa gtt tac att cct aag agg aag tcc aaa gtc	480
Ser Leu Asp Asn Asp Glu Val Tyr Ile Pro Lys Arg Lys Ser Lys Val	
145 150 155 160	
aag atc tac tcc aaa atc cta aac aac cca cct gga agg gtg ttc act	528
Lys Ile Tyr Ser Lys Ile Leu Asn Asn Pro Pro Gly Arg Val Phe Thr	
165 170 175	
ttg gtt ttc agg ttg act cta ggg ttt cct ttg tac ctg tta act aat	576
Leu Val Phe Arg Leu Thr Leu Gly Phe Pro Leu Tyr Leu Leu Thr Asn	
180 185 190	
atc tct gga aag aaa tac caa agg ttt gcc aac cac ttt gat cca ttg	624
Ile Ser Gly Lys Lys Tyr Gln Arg Phe Ala Asn His Phe Asp Pro Leu	
195 200 205	
agt ccc atc ttc acc gag agg gaa agg att cag gtt ctt gta tca gat	672

Ser Pro Ile Phe Thr Glu Arg Glu Arg Ile Gln Val Leu Val Ser Asp  
 210 215 220

ctt ggt ctt cta gct gta atc tac gca atc aag ctt ctt gtt gct gca 720  
 Leu Gly Leu Leu Ala Val Ile Tyr Ala Ile Lys Leu Leu Val Ala Ala  
 225 230 235 240

aaa gga gct gtc tgg gtg aca tgc atc tat gga gtt cca gtc cta ggt 768  
 Lys Gly Ala Val Trp Val Thr Cys Ile Tyr Gly Val Pro Val Leu Gly  
 245 250 255

gta agc gtg ttc ttc gtt ttg atc act tac ttg cac cac acc cat ctt 816  
 Val Ser Val Phe Phe Val Leu Ile Thr Tyr Leu His His Thr His Leu  
 260 265 270

tcc ttg cct cat tac gat tct act gag tgg aac tgg atc aga ggg gca 864  
 Ser Leu Pro His Tyr Asp Ser Thr Glu Trp Asn Trp Ile Arg Gly Ala  
 275 280 285

ttg tca acc atc gat agg gat ttt ggg ttc cta aat agg gtt ttc cat 912  
 Leu Ser Thr Ile Asp Arg Asp Phe Gly Phe Leu Asn Arg Val Phe His  
 290 295 300

gac gtt aca cac act cat gta ttg cat cat ttg atc tct tac att cca 960  
 Asp Val Thr His Thr His Val Leu His His Leu Ile Ser Tyr Ile Pro  
 305 310 315 320

cac tat cat gca aag gag gca aga gat gca atc aaa cca gtt ttg ggt 1008  
 His Tyr His Ala Lys Glu Ala Arg Asp Ala Ile Lys Pro Val Leu Gly  
 325 330 335

gat tat tat aag att gat agg act cct ata ttc aaa gca atg tgg aga 1056  
 Asp Tyr Tyr Lys Ile Asp Arg Thr Pro Ile Phe Lys Ala Met Trp Arg  
 340 345 350

gag gcc aag gaa tgc atc tat atc gag cca gat gaa gat act gaa cac 1104  
 Glu Ala Lys Glu Cys Ile Tyr Ile Glu Pro Asp Glu Asp Thr Glu His  
 355 360 365

aag ggt gtt tac tgg tac cat aaa atg taa 1134  
 Lys Gly Val Tyr Trp Tyr His Lys Met  
 370 375

<210> 34

<211> 383

<212> PRT

<213> Ricinus communis

<400> 34

Met Gly Gly Gly Gly Arg Met Ser Thr Val Ile Thr Ser Asn Asn Ser  
 1 5 10 15  
 Glu Ser Ser His Leu Lys Arg Ala Pro His Thr Lys Pro Pro Phe Thr  
 20 25 30  
 Leu Gly Asp Leu Lys Arg Ala Ile Pro Pro His Cys Phe Glu Arg Ser  
 35 40 45  
 Phe Val Arg Ser Phe Ser Tyr Val Ala Tyr Asp Val Cys Leu Ser Phe  
 50 55 60

Leu Phe Tyr Ser Ile Ala Thr Asn Phe Phe Pro Tyr Ile Ser Ser Pro  
 65 70 75 80  
 Leu Ser Tyr Val Ala Trp Leu Val Tyr Trp Leu Phe Gln Gly Cys Ile  
 85 90 95  
 Leu Thr Gly Leu Trp Val Ile Gly His Glu Cys Gly His His Ala Phe  
 100 105 110  
 Ser Glu Tyr Gln Leu Ala Asp Asp Ile Val Gly Leu Ile Val His Ser  
 115 120 125  
 Ala Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg His  
 130 135 140  
 His Ser Asn Ile Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys  
 145 150 155 160  
 Ser Lys Ser Lys Ile Ser Trp Tyr Ser Lys Tyr Leu Asn Asn Pro Pro  
 165 170 175  
 Gly Arg Val Leu Thr Leu Ala Ala Thr Leu Leu Leu Gly Trp Pro Leu  
 180 185 190  
 Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Arg Phe Ala Cys  
 195 200 205  
 His Tyr Asp Pro Tyr Gly Pro Ile Phe Ser Glu Arg Glu Arg Leu Gln  
 210 215 220  
 Ile Tyr Ile Ala Asp Leu Gly Ile Phe Ala Thr Thr Phe Val Leu Tyr  
 225 230 235 240  
 Gln Ala Thr Met Ala Lys Gly Leu Ala Trp Val Met Arg Ile Tyr Gly  
 245 250 255  
 Val Pro Leu Leu Ile Val Asn Cys Phe Leu Val Met Ile Thr Tyr Leu  
 260 265 270  
 Gln His Thr His Pro Ala Ile Pro Arg Tyr Gly Ser Ser Glu Trp Asp  
 275 280 285  
 Trp Leu Arg Gly Ala Met Val Thr Val Asp Arg Asp Tyr Gly Val Leu  
 290 295 300  
 Asn Lys Val Phe His Asn Ile Ala Asp Thr His Val Ala His His Leu  
 305 310 315 320  
 Phe Ala Thr Val Pro His Tyr His Ala Met Glu Ala Thr Lys Ala Ile  
 325 330 335  
 Lys Pro Ile Met Gly Glu Tyr Tyr Arg Tyr Asp Gly Thr Pro Phe Tyr  
 340 345 350  
 Lys Ala Leu Trp Arg Glu Ala Lys Glu Cys Leu Phe Val Glu Pro Asp  
 355 360 365  
 Glu Gly Ala Pro Thr Gln Gly Val Phe Trp Tyr Arg Asn Lys Tyr  
 370 375 380

<210> 35

<211> 383

<212> PRT

<213> *Lesquerella gracilis* B

<400> 35

Met Gly Ala Gly Gly Arg Ile Met Val Thr Pro Ser Ser Lys Lys Ser  
 1 5 10 15  
 Glu Thr Glu Ala Leu Lys Arg Gly Pro Cys Glu Lys Pro Pro Phe Thr  
 20 25 30  
 Val Lys Asp Leu Lys Lys Ala Ile Pro Gln His Cys Phe Gln Arg Ser  
 35 40 45  
 Ile Pro Arg Ser Phe Ser Tyr Leu Leu Thr Asp Ile Thr Leu Val Ser  
 50 55 60  
 Cys Phe Tyr Tyr Val Ala Thr Asn Tyr Phe Ser Leu Leu Pro Gln Pro  
 65 70 75 80

Leu Ser Tyr Leu Ala Trp Pro Leu Tyr Trp Val Cys Gln Gly Cys Val  
 85 90 95  
 Leu Thr Gly Ile Trp Val Leu Gly His Glu Cys Gly His His Ala Phe  
 100 105 110  
 Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Phe Ile Phe His Ser  
 115 120 125  
 Leu Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg His  
 130 135 140  
 His Ser Asn Asn Gly Ser Leu Glu Lys Asp Glu Val Phe Val Pro Pro  
 145 150 155 160  
 Lys Lys Ala Ala Val Lys Trp Tyr Val Lys Tyr Leu Asn Asn Pro Leu  
 165 170 175  
 Gly Arg Ile Leu Val Leu Thr Val Arg Phe Ile Leu Gly Trp Pro Leu  
 180 185 190  
 Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Phe Ala Ser  
 195 200 205  
 His Phe Phe Pro His Ala Pro Ile Phe Lys Asp Arg Glu Arg Leu Gln  
 210 215 220  
 Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu Tyr  
 225 230 235 240  
 Arg Tyr Ala Ala Ser Gln Gly Leu Thr Ala Met Ile Cys Val Tyr Gly  
 245 250 255  
 Val Pro Leu Leu Ile Val Asn Phe Phe Leu Val Leu Val Thr Phe Leu  
 260 265 270  
 Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Thr Glu Trp Glu  
 275 280 285  
 Trp Ile Arg Gly Ala Leu Val Thr Val Asp Arg Asp Tyr Gly Ile Leu  
 290 295 300  
 Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His Leu  
 305 310 315 320  
 Phe Ala Thr Ile Pro His Tyr Asn Ala Met Glu Ala Thr Glu Ala Ile  
 325 330 335  
 Lys Pro Ile Leu Gly Asp Tyr Tyr His Phe Asp Gly Thr Pro Trp Tyr  
 340 345 350  
 Val Ala Met Tyr Arg Glu Ala Lys Glu Cys Leu Tyr Val Glu Pro Asp  
 355 360 365  
 Thr Glu Arg Gly Lys Lys Gly Val Tyr Tyr Tyr Asn Asn Lys Leu  
 370 375 380

&lt;210&gt; 36

&lt;211&gt; 377

&lt;212&gt; PRT

&lt;213&gt; Stokesia laevis

&lt;400&gt; 36

Met Gly Ala Gly Gly Arg Met Ser Asp Leu Ser Asp Gly Lys Asn Leu  
 1 5 10 15  
 Leu Lys Arg Val Pro Val Asp Pro Pro Phe Thr Leu Ser Asp Ile Lys  
 20 25 30  
 Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser Val Ile Arg Ser Ser  
 35 40 45  
 Tyr Tyr Val Val His Asp Leu Ile Val Ser Tyr Val Phe Phe Phe Leu  
 50 55 60  
 Ala Thr Thr Tyr Ile Thr Val Leu Pro Ala Pro Leu Ala Tyr Ile Ala  
 65 70 75 80  
 Trp Pro Val Tyr Trp Phe Cys Gln Ala Ser Ile Leu Thr Gly Leu Trp  
 85 90 95

Val Ile Gly His Glu Cys Gly His His Ala Phe Ser Glu Tyr Gln Trp  
 100 105 110  
 Ile Asp Asp Thr Val Gly Phe Ile Leu His Ser Ala Leu Leu Thr Pro  
 115 120 125  
 Tyr Phe Ser Trp Lys Tyr Ser His Arg Asn His His Ala Asn Thr Asn  
 130 135 140  
 Ser Leu Asp Asn Asp Glu Val Tyr Ile Pro Lys Arg Lys Ser Lys Val  
 145 150 155 160  
 Lys Ile Tyr Ser Lys Ile Leu Asn Asn Pro Pro Gly Arg Val Phe Thr  
 165 170 175  
 Leu Val Phe Arg Leu Thr Leu Gly Phe Pro Leu Tyr Leu Leu Thr Asn  
 180 185 190  
 Ile Ser Gly Lys Lys Tyr Gln Arg Phe Ala Asn His Phe Asp Pro Leu  
 195 200 205  
 Ser Pro Ile Phe Thr Glu Arg Glu Arg Ile Gln Val Leu Val Ser Asp  
 210 215 220  
 Leu Gly Leu Leu Ala Val Ile Tyr Ala Ile Lys Leu Leu Val Ala Ala  
 225 230 235 240  
 Lys Gly Ala Val Trp Val Thr Cys Ile Tyr Gly Val Pro Val Leu Gly  
 245 250 255  
 Val Ser Val Phe Phe Val Leu Ile Thr Tyr Leu His His Thr His Leu  
 260 265 270  
 Ser Leu Pro His Tyr Asp Ser Thr Glu Trp Asn Trp Ile Arg Gly Ala  
 275 280 285  
 Leu Ser Thr Ile Asp Arg Asp Phe Gly Phe Leu Asn Arg Val Phe His  
 290 295 300  
 Asp Val Thr His Thr His Val Leu His His Leu Ile Ser Tyr Ile Pro  
 305 310 315 320  
 His Tyr His Ala Lys Glu Ala Arg Asp Ala Ile Lys Pro Val Leu Gly  
 325 330 335  
 Asp Tyr Tyr Lys Ile Asp Arg Thr Pro Ile Phe Lys Ala Met Trp Arg  
 340 345 350  
 Glu Ala Lys Glu Cys Ile Tyr Ile Glu Pro Asp Glu Asp Thr Glu His  
 355 360 365  
 Lys Gly Val Tyr Trp Tyr His Lys Met  
 370 375

<210> 37

<211> 387

<212> PRT

<213> Ricinus communis

<400> 37

Met Ala Ser Ser Gly Arg Met Ser Thr Val Ile Thr Ser Asn Asn Ser  
 1 5 10 15  
 Glu Lys Lys Gly Gly Ser Ser His Leu Lys Arg Ala Pro His Thr Lys  
 20 25 30  
 Pro Pro Phe Thr Leu Gly Asp Leu Lys Arg Ala Ile Pro Pro His Cys  
 35 40 45  
 Phe Glu Arg Ser Phe Val Arg Ser Phe Ser Tyr Val Ala Tyr Asp Val  
 50 55 60  
 Cys Leu Ser Phe Leu Phe Tyr Ser Ile Ala Thr Asn Phe Phe Pro Tyr  
 65 70 75 80  
 Ile Ser Ser Pro Leu Ser Tyr Val Ala Trp Leu Val Tyr Trp Leu Phe  
 85 90 95  
 Gln Gly Cys Ile Leu Thr Gly Leu Trp Val Ile Gly His Glu Cys Gly  
 100 105 110

His His Ala Phe Ser Glu Tyr Gln Leu Ala Asp Asp Ile Val Gly Leu  
 115 120 125  
 Ile Val His Ser Ala Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser  
 130 135 140  
 His Arg Arg His His Ser Asn Ile Gly Ser Leu Glu Arg Asp Glu Val  
 145 150 155 160  
 Phe Val Pro Lys Ser Lys Ser Lys Ile Ser Trp Tyr Ser Lys Tyr Leu  
 165 170 175  
 Asn Asn Pro Pro Gly Arg Val Leu Thr Leu Ala Ala Thr Leu Leu Leu  
 180 185 190  
 Gly Trp Pro Leu Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp  
 195 200 205  
 Arg Phe Ala Cys His Tyr Asp Pro Tyr Gly Pro Ile Phe Ser Glu Arg  
 210 215 220  
 Glu Arg Leu Gln Ile Tyr Ile Ala Asp Leu Gly Ile Phe Ala Thr Thr  
 225 230 235 240  
 Phe Val Leu Tyr Gln Ala Thr Met Ala Lys Gly Leu Ala Trp Val Met  
 245 250 255  
 Arg Ile Tyr Gly Val Pro Leu Leu Ile Val Asn Cys Phe Leu Val Met  
 260 265 270  
 Ile Thr Tyr Leu Gln His Thr His Pro Ala Ile Pro Arg Tyr Gly Ser  
 275 280 285  
 Ser Glu Trp Asp Trp Leu Arg Gly Ala Met Val Thr Val Asp Arg Asp  
 290 295 300  
 Tyr Gly Val Leu Asn Lys Val Phe His Asn Ile Ala Asp Thr His Val  
 305 310 315 320  
 Ala His His Leu Phe Ala Thr Val Pro His Tyr His Ala Met Glu Ala  
 325 330 335  
 Thr Lys Ala Ile Lys Pro Ile Met Gly Glu Tyr Tyr Arg Tyr Asp Gly  
 340 345 350  
 Thr Pro Phe Tyr Lys Ala Leu Trp Arg Glu Ala Lys Glu Cys Leu Phe  
 355 360 365  
 Val Glu Pro Asp Glu Gly Ala Pro Thr Gln Gly Val Phe Trp Tyr Arg  
 370 375 380  
 Asn Lys Tyr  
 385

<210> 38

<211> 377

<212> PRT

<213> Stokesia laevis

<400> 38

Met Ala Ser Ser Gly Arg Met Ser Asp Leu Ser Asp Gly Lys Asn Leu  
 1 5 10 15  
 Leu Lys Arg Val Pro Val Asp Pro Pro Phe Thr Leu Ser Asp Ile Lys  
 20 25 30  
 Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser Val Ile Arg Ser Ser  
 35 40 45  
 Tyr Tyr Val Val His Asp Leu Ile Val Ser Tyr Val Phe Phe Phe Leu  
 50 55 60  
 Ala Thr Thr Tyr Ile Thr Val Leu Pro Ala Pro Leu Ala Tyr Ile Ala  
 65 70 75 80  
 Trp Pro Val Tyr Trp Phe Cys Gln Ala Ser Ile Leu Thr Gly Leu Trp  
 85 90 95  
 Val Ile Gly His Glu Cys Gly His His Ala Phe Ser Glu Tyr Gln Trp  
 100 105 110



Ile Asp Asp Thr Val Gly Phe Ile Leu His Ser Ala Leu Leu Thr Pro  
 115 120 125  
 Tyr Phe Ser Trp Lys Tyr Ser His Arg Asn His His Ala Asn Thr Asn  
 130 135 140  
 Ser Leu Asp Asn Asp Glu Val Tyr Ile Pro Lys Arg Lys Ser Lys Val  
 145 150 155 160  
 Lys Ile Tyr Ser Lys Ile Leu Asn Asn Pro Pro Gly Arg Val Phe Thr  
 165 170 175  
 Leu Val Phe Arg Leu Thr Leu Gly Phe Pro Leu Tyr Leu Leu Thr Asn  
 180 185 190  
 Ile Ser Gly Lys Lys Tyr Gln Arg Phe Ala Asn His Phe Asp Pro Leu  
 195 200 205  
 Ser Pro Ile Phe Thr Glu Arg Glu Arg Ile Gln Val Leu Val Ser Asp  
 210 215 220  
 Leu Gly Leu Leu Ala Val Ile Tyr Ala Ile Lys Leu Leu Val Ala Ala  
 225 230 235 240  
 Lys Gly Ala Val Trp Val Thr Cys Ile Tyr Gly Val Pro Val Leu Gly  
 245 250 255  
 Val Ser Val Phe Phe Val Leu Ile Thr Tyr Leu His His Thr His Leu  
 260 265 270  
 Ser Leu Pro His Tyr Asp Ser Thr Glu Trp Asn Trp Ile Arg Gly Ala  
 275 280 285  
 Leu Ser Thr Ile Asp Arg Asp Phe Gly Phe Leu Asn Arg Val Phe His  
 290 295 300  
 Asp Val Thr His Thr His Val Leu His His Leu Ile Ser Tyr Ile Pro  
 305 310 315 320  
 His Tyr His Ala Lys Glu Ala Arg Asp Ala Ile Lys Pro Val Leu Gly  
 325 330 335  
 Asp Tyr Tyr Lys Ile Asp Arg Thr Pro Ile Phe Lys Ala Met Trp Arg  
 340 345 350  
 Glu Ala Lys Glu Cys Ile Tyr Ile Glu Pro Asp Glu Asp Thr Glu His  
 355 360 365  
 Lys Gly Val Tyr Trp Tyr His Lys Met  
 370 375

<210> 39

<211> 387

<212> PRT

<213> Ricinus communis

<400> 39

Met Ala Ser Ser Gly Arg Met Ser Thr Val Ile Thr Ser Asn Asn Ser  
 1 5 10 15  
 Glu Lys Lys Gly Gly Ser Ser His Leu Lys Arg Ala Pro His Thr Lys  
 20 25 30  
 Pro Pro Phe Thr Leu Gly Asp Leu Lys Arg Ala Ile Pro Pro His Cys  
 35 40 45  
 Phe Glu Arg Ser Phe Val Arg Ser Phe Ser Tyr Val Ala Tyr Asp Val  
 50 55 60  
 Cys Leu Ser Phe Leu Phe Tyr Ser Ile Ala Thr Asn Phe Phe Pro Tyr  
 65 70 75 80  
 Ile Ser Ser Pro Leu Ser Tyr Val Ala Trp Leu Val Tyr Trp Leu Phe  
 85 90 95  
 Gln Gly Cys Ile Leu Thr Gly Leu Trp Val Ile Gly His Glu Cys Gly  
 100 105 110  
 His His Ala Phe Ser Glu Tyr Gln Leu Ala Asp Asp Ile Val Gly Leu  
 115 120 125

Ile Val His Ser Ala Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser  
 130 135 140  
 His Arg Arg His His Ser Asn Ile Gly Ser Leu Glu Arg Asp Glu Val  
 145 150 155 160  
 Phe Val Pro Lys Ser Lys Ser Lys Ile Ser Trp Tyr Ser Lys Tyr Leu  
 165 170 175  
 Asn Asn Pro Pro Gly Arg Val Leu Thr Leu Ala Ala Thr Leu Leu Leu  
 180 185 190  
 Gly Trp Pro Leu Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp  
 195 200 205  
 Arg Phe Ala Cys His Tyr Asp Pro Tyr Gly Pro Ile Phe Ser Glu Arg  
 210 215 220  
 Glu Arg Leu Gln Ile Tyr Ile Ala Asp Leu Gly Ile Phe Ala Thr Thr  
 225 230 235 240  
 Phe Val Leu Tyr Gln Ala Thr Met Ala Lys Gly Leu Ala Trp Val Met  
 245 250 255  
 Arg Ile Tyr Gly Val Pro Leu Leu Ile Val Asn Cys Phe Leu Val Met  
 260 265 270  
 Ile Thr Tyr Leu Gln His Thr His Pro Ala Ile Pro Arg Tyr Gly Ser  
 275 280 285  
 Ser Glu Trp Asp Trp Leu Arg Gly Ala Met Val Thr Val Asp Arg Asp  
 290 295 300  
 Tyr Gly Val Leu Asn Lys Val Phe His Asn Ile Ala Asp Thr His Val  
 305 310 315 320  
 Ala His His Leu Phe Ala Thr Val Pro His Tyr His Ala Met Glu Ala  
 325 330 335  
 Thr Lys Ala Ile Lys Pro Ile Met Gly Glu Tyr Tyr Arg Tyr Asp Gly  
 340 345 350  
 Thr Pro Phe Tyr Lys Ala Leu Trp Arg Glu Ala Lys Glu Cys Leu Phe  
 355 360 365  
 Val Glu Pro Asp Glu Gly Ala Pro Thr Gln Gly Val Phe Trp Tyr Arg  
 370 375 380  
 Asn Lys Tyr  
 385

<210> 40

<211> 384

<212> PRT

<213> Artificial Sequence

<220>

<223> hypothetical sequence

<400> 40

Met Ala Ser Ser Gly Arg Ile Met Val Thr Pro Ser Ser Lys Lys Ser  
 1 5 10 15  
 Glu Thr Glu Ala Leu Lys Arg Gly Pro Cys Glu Lys Pro Pro Phe Thr  
 20 25 30  
 Val Lys Asp Leu Lys Lys Ala Ile Pro Gln His Cys Phe Gln Arg Ser  
 35 40 45  
 Ile Pro Arg Ser Phe Ser Tyr Leu Leu Thr Asp Ile Thr Leu Val Ser  
 50 55 60  
 Cys Phe Tyr Tyr Val Ala Thr Asn Tyr Phe Ser Leu Leu Pro Gln Pro  
 65 70 75 80  
 Leu Ser Thr Tyr Leu Ala Trp Pro Leu Tyr Trp Val Cys Gln Gly Cys  
 85 90 95  
 Val Leu Thr Gly Ile Trp Val Leu Gly His Glu Cys Gly His His Ala

			100					105				110			
Phe	Ser	Asp	Tyr	Gln	Trp	Leu	Asp	Asp	Thr	Val	Gly	Phe	Ile	Phe	His
			115					120					125		
Ser	Leu	Leu	Leu	Val	Pro	Tyr	Phe	Ser	Trp	Lys	Tyr	Ser	His	Arg	Arg
			130					135					140		
His	His	Ser	Asn	Asn	Gly	Ser	Leu	Glu	Lys	Asp	Glu	Val	Phe	Val	Pro
145					150					155					160
Pro	Lys	Lys	Ala	Ala	Val	Lys	Trp	Tyr	Val	Lys	Tyr	Leu	Asn	Asn	Pro
				165						170					175
Leu	Gly	Arg	Ile	Leu	Val	Leu	Thr	Val	Arg	Phe	Ile	Leu	Gly	Trp	Pro
			180						185					190	
Leu	Tyr	Leu	Ala	Phe	Asn	Val	Ser	Gly	Arg	Pro	Tyr	Asp	Gly	Phe	Ala
			195					200					205		
Ser	His	Phe	Phe	Pro	His	Ala	Pro	Ile	Phe	Lys	Asp	Arg	Glu	Arg	Leu
						215						220			
Gln	Ile	Tyr	Ile	Ser	Asp	Ala	Gly	Ile	Leu	Ala	Val	Cys	Tyr	Gly	Leu
225					230					235					240
Tyr	Arg	Tyr	Ala	Ala	Ser	Gln	Gly	Leu	Thr	Ala	Met	Ile	Cys	Val	Tyr
				245						250				255	
Gly	Val	Pro	Leu	Leu	Ile	Val	Asn	Phe	Phe	Leu	Val	Leu	Val	Thr	Phe
				260					265					270	
Leu	Gln	His	Thr	His	Pro	Ser	Leu	Pro	His	Tyr	Asp	Ser	Thr	Glu	Trp
			275					280					285		
Glu	Trp	Ile	Arg	Gly	Ala	Leu	Val	Thr	Val	Asp	Arg	Asp	Tyr	Gly	Ile
						295					300				
Leu	Asn	Lys	Val	Phe	His	Asn	Ile	Thr	Asp	Thr	His	Val	Ala	His	His
305					310					315					320
Leu	Phe	Ala	Thr	Ile	Pro	His	Tyr	Asn	Ala	Met	Glu	Ala	Thr	Glu	Ala
				325					330					335	
Ile	Lys	Pro	Ile	Leu	Gly	Asp	Tyr	Tyr	His	Phe	Asp	Gly	Thr	Pro	Trp
				340					345					350	
Tyr	Val	Ala	Met	Tyr	Arg	Glu	Ala	Lys	Glu	Cys	Leu	Tyr	Val	Glu	Pro
			355				360						365		
Asp	Thr	Glu	Arg	Gly	Lys	Lys	Gly	Val	Tyr	Tyr	Tyr	Asn	Asn	Lys	Leu
			370				375							380	

<210> 41

<211> 374

<212> PRT

<213> Artificial Sequence

<220>

<223> hypothetical sequence

<400> 41

Met	Ala	Ser	Ser	Gly	His	Ser	Arg	Thr	Ser	Lys	Lys	Ser	Val	Met	Glu
1				5					10					15	
Arg	Val	Ser	Val	Asp	Pro	Val	Pro	Phe	Ser	Leu	Ser	Asp	Leu	Lys	Gln
				20				25					30		
Ala	Ile	Pro	Pro	His	Cys	Phe	Gln	Arg	Ser	Val	Ile	Arg	Ser	Ser	Tyr
				35			40					45			
Tyr	Val	Val	His	Asp	Leu	Ile	Ile	Ala	Tyr	Ile	Phe	Tyr	Phe	Leu	Ala
				50		55					60				
Asp	Lys	Tyr	Ile	Pro	Ile	Leu	Pro	Ala	Pro	Leu	Ala	Tyr	Leu	Ala	Trp
65					70					75					80
Pro	Leu	Tyr	Trp	Phe	Cys	Gln	Ala	Ser	Ile	Leu	Thr	Gly	Leu	Trp	Ile
				85					90					95	

Leu Gly His Glu Cys Gly His His Ala Phe Ser Glu Tyr Gln Trp Val  
 100 105 110  
 Asp Asp Thr Val Gly Phe Met Val His Ser Phe Leu Leu Thr Pro Tyr  
 115 120 125  
 Phe Ser Trp Lys Tyr Ser His Arg Asn His His Ala Asn Thr Ser Ser  
 130 135 140  
 Ile Asp Asn Asp Glu Val Tyr Ile Pro Lys Ser Lys Ser Lys Leu Ala  
 145 150 155 160  
 Leu Thr Tyr Lys Leu Leu Asn Asn Pro Pro Gly Arg Leu Leu Val Met  
 165 170 175  
 Val Ile Met Phe Thr Leu Gly Phe Pro Leu Tyr Leu Leu Thr Asn Ile  
 180 185 190  
 Ser Gly Lys Lys Tyr Asp Arg Phe Ala Asn His Phe Asp Pro Met Ser  
 195 200 205  
 Pro Ile Phe Lys Glu Arg Glu Arg Phe Gln Val Leu Leu Ser Asp Leu  
 210 215 220  
 Gly Leu Leu Ala Val Phe Tyr Gly Ile Lys Val Ala Val Ala Lys Lys  
 225 230 235 240  
 Gly Ala Ala Trp Val Ala Cys Met Tyr Gly Val Pro Met Leu Gly Val  
 245 250 255  
 Phe Thr Leu Phe Asp Ile Ile Thr Tyr Leu His His Thr His Gln Ser  
 260 265 270  
 Ser Pro His Tyr Asp Ser Thr Glu Trp Asn Trp Ile Arg Gly Ala Leu  
 275 280 285  
 Ser Ala Ile Asp Arg Asp Phe Gly Phe Met Asn Ser Val Phe His Asp  
 290 295 300  
 Val Thr His Thr His Val Met His His Met Phe Ser Tyr Ile Pro His  
 305 310 315 320  
 Tyr His Ala Lys Glu Ala Arg Asp Ala Ile Asn Thr Ile Ile Gly Asp  
 325 330 335  
 Tyr Tyr Met Ile Asp Arg Thr Pro Ile Leu Lys Ala Leu Trp Arg Glu  
 340 345 350  
 Ala Lys Glu Cys Met Tyr Ile Glu Pro Asp Ser Lys Arg Lys Gly Val  
 355 360 365  
 Tyr Trp Tyr His Lys Leu  
 370

<210> 42

<211> 377

<212> PRT

<213> Stokesia laevis

<400> 42

Met Ala Ser Ser Gly Arg Met Ser Asp Leu Ser Asp Gly Lys Asn Leu  
 1 5 10 15  
 Leu Lys Arg Val Pro Val Asp Pro Pro Phe Thr Leu Ser Asp Ile Lys  
 20 25 30  
 Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser Val Ile Arg Ser Ser  
 35 40 45  
 Tyr Tyr Val Val His Asp Leu Ile Val Ser Tyr Val Phe Phe Leu  
 50 55 60  
 Ala Thr Thr Tyr Ile Thr Val Leu Pro Ala Pro Leu Ala Tyr Ile Ala  
 65 70 75 80  
 Trp Pro Val Tyr Trp Phe Cys Gln Ala Ser Ile Leu Thr Gly Leu Trp  
 85 90 95  
 Val Ile Gly His Glu Cys Gly His His Ala Phe Ser Glu Tyr Gln Trp  
 100 105 110

Ile Asp Asp Thr Val Gly Phe Ile Leu His Ser Ala Leu Leu Thr Pro  
 115 120 125  
 Tyr Phe Ser Trp Lys Tyr Ser His Arg Asn His His Ala Asn Thr Asn  
 130 135 140  
 Ser Leu Asp Asn Asp Glu Val Tyr Ile Pro Lys Arg Lys Ser Lys Val  
 145 150 155 160  
 Lys Ile Tyr Ser Lys Ile Leu Asn Asn Pro Pro Gly Arg Val Phe Thr  
 165 170 175  
 Leu Val Phe Arg Leu Thr Leu Gly Phe Pro Leu Tyr Leu Leu Thr Asn  
 180 185 190  
 Ile Ser Gly Lys Lys Tyr Gln Arg Phe Ala Asn His Phe Asp Pro Leu  
 195 200 205  
 Ser Pro Ile Phe Thr Glu Arg Glu Arg Ile Gln Val Leu Val Ser Asp  
 210 215 220  
 Leu Gly Leu Leu Ala Val Ile Tyr Ala Ile Lys Leu Leu Val Ala Ala  
 225 230 235 240  
 Lys Gly Ala Val Trp Val Thr Cys Ile Tyr Gly Val Pro Val Leu Gly  
 245 250 255  
 Val Ser Val Phe Phe Val Leu Ile Thr Tyr Leu His His Thr His Leu  
 260 265 270  
 Ser Leu Pro His Tyr Asp Ser Thr Glu Trp Asn Trp Ile Arg Gly Ala  
 275 280 285  
 Leu Ser Thr Ile Asp Arg Asp Phe Gly Phe Leu Asn Arg Val Phe His  
 290 295 300  
 Asp Val Thr His Thr His Val Leu His His Leu Ile Ser Tyr Ile Pro  
 305 310 315 320  
 His Tyr His Ala Lys Glu Ala Arg Asp Ala Ile Lys Pro Val Leu Gly  
 325 330 335  
 Asp Tyr Tyr Lys Ile Asp Arg Thr Pro Ile Phe Lys Ala Met Trp Arg  
 340 345 350  
 Glu Ala Lys Glu Cys Ile Tyr Ile Glu Pro Asp Glu Asp Thr Glu His  
 355 360 365  
 Lys Gly Val Tyr Trp Tyr His Lys Met  
 370 375

<210> 43

<211> 92

<212> DNA

<213> Arabidopsis thaliana

<400> 43

agagagagag attctgcgga ggagcttctt cttcgtaggg tgttcacgtg tattaacggt 60  
 atcgccccta cgtcagctcc atctccagaa ac 92

<210> 44

<211> 1222

<212> DNA

<213> Arabidopsis thaliana

<400> 44

agagagagag attctgcgga ggagcttctt cttcgtaggg tgttcacgtg tattaacggt 60  
 atcgccccta cgtcagctcc atctccaggt cgcgcttc tcttccattt cttctcattt 120  
 tcgattttga ttcttatttc tttccagtag ctctgctct gtgaatttct cgcctcacga 180  
 tagatctgct tatactcctt acattcaacc ttagatctgg tctcgattct ctgtttctct 240  
 gtttttttct tttggctgag aatctgatgt ttgtttatgt tctgtcacca ttaataataa 300  
 tgaactctct cattcataca atgattagtt tctctcgtct acaaaacgat atgttgcatt 360  
 ttcacttttc ttcttttttt ctaagatgat ttgctttgac caatttgttt agatctttat 420

tctat	tttct	ggtgg	gttgg	tgga	attg	aaaaa	aaaaa	cagc	ataa	attg	480				
atttg	tta	gtatt	cattt	tttgg	ctatt	tg	tct	gggt	aaaa	atctgc	ttct	actatt	540		
gaatc	tttcc	tggat	ttttt	actc	ctattg	gg	tttt	tata	gt	aaaa	aatac	ataa	taaa	aaag	600
gaaa	caaaa	gtttt	ataga	ttct	cttaa	ccc	cttac	ga	t	aaa	agttg	aat	caaaa	ata	660
attc	aggatc	agat	gctctt	tgat	tgattc	agat	gcgatt	acag	ttgcat	gg	caa	atttt	720		
ctagat	ccgt	cgtc	acattt	tatt	ttctgt	ttaa	atatct	aaat	ctgata	tat	gatg	tcg	780		
acaa	attctg	gtgg	cttata	catc	acttca	actg	ttttct	ttt	ggcttg	ttt	gtca	act	840		
tggt	tttcaa	tacg	atttgt	gatt	tcgatc	gctg	aat	ttt	taata	caagc	aa	actgat	900		
taacc	acaag	caag	agatgt	gac	ctgcctt	atta	acatcg	tatt	acttac	tact	agtc	960			
attct	caacg	caat	cgtttt	tgt	atttctc	acatt	atgcc	gct	tctctac	tct	tatt	1020			
tttt	ggtcca	cg	cattttct	att	gtggca	atcc	cttca	caac	ctgatt	tccc	actttg	1080			
gatc	atttgt	ctga	agactc	tct	tgaatcg	ttacc	acttg	ttt	cttgtgc	atg	ctctgtt	1140			
tttt	agaatt	aatg	ataaaa	ctatt	ccata	gtct	ttagtt	ttc	agcttgt	tgatt	ctttt	1200			
gct	tttgg	ttct	gcagaa	ac								1222			

<210> 45

<211> 222

<212> DNA

<213> Arabidopsis thaliana

<400> 45

ggat	gatgg	gaaga	aattg	tcgac	ctttc	tctt	gtctgt	ttgt	cttttg	ttaa	agaagc	60
tatg	cttcg	ttta	ataatc	ttatt	gtcca	tttt	gttgtg	ttat	gacatt	ttgg	ctgctc	120
attat	gttat	gtgg	gaagtt	agt	gttcaaa	tg	ttttgtgt	cg	gattg	ctt	ctcatcg	180
ctg	ttttgtt	ggg	atcgtag	aat	gtgacc	ttc	ggacagt	aa				222

<210> 46

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 46

atggg	aggtg	gtgg	tcgcat	g								21
-------	-------	------	--------	---	--	--	--	--	--	--	--	----

<210> 47

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 47

tta	aacttg	ttcc	ggtacc	a								21
-----	--------	------	--------	---	--	--	--	--	--	--	--	----

<210> 48

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 48

atgggtgctg gtggaagaat aatg 24

<210> 49  
 <211> 33  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> primer

<400> 49  
 tcataactta ttgaagtaat agtagacacc ttt 33

<210> 50  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> primer

<400> 50  
 tcataactta ttggtgtaat a 21

<210> 51  
 <211> 17  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> primer

<400> 51  
 gcaatccctc cccattg 17

<210> 52  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> primer

<400> 52  
 tcacaattta tcataccaat aaacacc 27

<210> 53  
 <211> 32  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> primer

<400> 53  
 atacaaaagc ttagagagag agattctgcg ga 32

<210> 54  
 <211> 33  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> primer

<400> 54  
 attcaatgca tgcaacataa tgagcagcca aaa 33

<210> 55  
 <211> 33  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> primer

<400> 55  
 attcaataag cttatgggtg caggtggaag aat 33

<210> 56  
 <211> 32  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> primer

<400> 56  
 atacaagcat gctcataact tattgttgta cc 32

<210> 57  
 <211> 40  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> primer

<400> 57  
 aagcaatggg gtgggatggc tttcttcaga tctcccaccg 40

<210> 58  
 <211> 40  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> primer

<400> 58  
 cgggtgggaga totgaagaaa gccatcccac cccattgctt 40

<210> 59  
 <211> 26



<212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> primer  
  
 <400> 59  
 gtcgacatac ttgttccggt accaga 26  
  
 <210> 60  
 <211> 39  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> primer  
  
 <400> 60  
 cgattgcttt cttcagatct cccaccgaga aaggcggtt 39  
  
 <210> 61  
 <211> 39  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> primer  
  
 <400> 61  
 aaccgccttt ctcggtggga gatctgaaga aagcaatcc 39  
  
 <210> 62  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> primer  
  
 <400> 62  
 gtcgactaac ttattgttgt aatagt 26  
  
 <210> 63  
 <211> 40  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> primer  
  
 <400> 63  
 gggattgctt tccttagatc tcccaccgag aaaggcggtt 40  
  
 <210> 64  
 <211> 40  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> primer

<400> 64

aaccgccttt ctcggtggga gatctaagga aagcaatccc 40

<210> 65

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 65

gtcgactaac ttattgttgt aatagt 26

<210> 66

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 66

aaccgccttt ctcggtggga gatctgaaga aagcaatccc 40

<210> 67

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 67

gggattgctt tcttcagatc tcccaccgag aaaggcggtt 40

<210> 68

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 68

gtcgactcat aacttattgt tgtaat 26

<210> 69

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 69

cgggtgggaga tctgaagaaa gcaatccctc cccattgctt

40

<210> 70

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 70

aagcaatggg gagggattgc tttcttcaga tctcccaccg

40

<210> 71

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 71

gtcgaaccaat ttatgatacc aataaaa

26

<210> 72

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 72

atacaaaaagc ttataatggg aggtgggtggt cgcac

35

<210> 73

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 73

atacaaggat ccttaatact tgttccggta cc

32

<210> 74

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 74  
 atacaagcgg ccgcagcgta atctggaaca tcgt 34

<210> 75  
 <211> 35  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> primer

<400> 75  
 atacaaaagc ttataatggg tgctggtgga agaat 35

<210> 76  
 <211> 32  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> primer

<400> 76  
 atacaaggat cctcataact tattggtgta at 32

<210> 77  
 <211> 35  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> primer

<400> 77  
 atacaaaagc ttataatgta cccatagcat gttcc 35

<210> 78  
 <211> 34  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> primer

<400> 78  
 atgagagctc gtttaaacga ttttaatggt tagc 34

<210> 79  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> primer

<400> 79  
 atgagaattc ggccggccaa tagtctcgac 30

<210> 80  
 <211> 31  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> primer  
  
 <400> 80  
 tcatgaggcg cgccaaagca cataacttadc g 31  
  
 <210> 81  
 <211> 33  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> primer  
  
 <400> 81  
 atgagcatgc aagcttcttc gcctggagga gag 33  
  
 <210> 82  
 <211> 35  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> primer  
  
 <400> 82  
 agctatgtac ccatacgatg ttccagatta cgctg 35  
  
 <210> 83  
 <211> 35  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> primer  
  
 <400> 83  
 tcgacagcgt aatctggaac atcgtatggg tacat 35  
  
 <210> 84  
 <211> 47  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> primer  
  
 <400> 84  
 gatccatgta cccaatacga tgttccagat tacgctctcg aggagct 47  
  
 <210> 85

<211> 37  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> primer  
  
 <400> 85  
 ctcgagagcg taatctggaa catcgtatgg gtacatg 37  
  
 <210> 86  
 <211> 34  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> primer  
  
 <400> 86  
 atgaggcgcg ccctttctct gacttttaac atcc 34  
  
 <210> 87  
 <211> 36  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> primer  
  
 <400> 87  
 actggcatgc gtattgagat tgttttataa tatatg 36  
  
 <210> 88  
 <211> 32  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> primer  
  
 <400> 88  
 atacaaaagc ttatgggagg tgggtggtcgc at 32  
  
 <210> 89  
 <211> 32  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> primer  
  
 <400> 89  
 atacaaggat ccatacttgt tccggtacca ga 32  
  
 <210> 90  
 <211> 32  
 <212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 90

atacaaaaagc ttatgggtgc tgggtggaaga at

32

<210> 91

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 91

atacaaggat cctaacttat tgttgtaata gt

32

<210> 92

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 92

atacaagtcg acatgggagg tgggtggtcgc at

32

<210> 93

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 93

atacaaggat ccatacttgt tccggtacca ga

32

<210> 94

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 94

ataaccagca acaacagtga gagcagccac cttaagcgag c

41

<210> 95

<211> 41

<212> DNA

<213> Artificial Sequence

<220>  
 <223> primer  
  
 <400> 95  
 gctcgcttaa ggtggctgct ctcaactggtg ttgctgggta t 41  
  
 <210> 96  
 <211> 41  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> primer  
  
 <400> 96  
 ttcttctca gcctctctct tacctagctt ggcctctcta t 41  
  
 <210> 97  
 <211> 41  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> primer  
  
 <400> 97  
 atagagaggc caagctaggt aagagagagg ctgaggaaga a 41  
  
 <210> 98  
 <211> 34  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> primer  
  
 <400> 98  
 caattgtcta gattaatact tgttccggta ccag 34  
  
 <210> 99  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> primer  
  
 <400> 99  
 aagcttacca tgggaggtgg tggtcg 26  
  
 <210> 100  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> primer



<400> 100  
 gaaacagcta tgacccatg 18

<210> 101  
 <211> 34  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> primer

<400> 101  
 caattgtcta gatcataact tattggtgta atag 34

<210> 102  
 <211> 29  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> primer

<400> 102  
 aagcttacca tgggtgctgg tggaagaat 29

<210> 103  
 <211> 35  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> primer

<400> 103  
 caattgtcta gatcacaatt tatgatacca ataaa 35

<210> 104  
 <211> 34  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> primer

<400> 104  
 atacaaggat ccaaattggga ggtggtggtc gcat 34

<210> 105  
 <211> 34  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> primer

<400> 105

atacaaggat ccaaatgggt gctggtggaa gaat 34  
 <210> 106  
 <211> 32  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> primer  
 <400> 106  
 aggatcccta ccatgggtgc agtggtcgg at 32  
 <210> 107  
 <211> 29  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> primer  
 <400> 107  
 tctagattac attttatggt accagtaaa 29  
 <210> 108  
 <211> 31  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> primer  
 <400> 108  
 agatctctac catgggtgcc cacggccatg g 31  
 <210> 109  
 <211> 49  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> primer  
 <400> 109  
 agcttctcga gaccatggcg taccgtagc acgtgcccga ctaccgag 49  
 <210> 110  
 <211> 49  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> primer  
 <400> 110  
 gatcctggcg tagtcgggca cgtcgtacgg gtaccgcatg gtctcgaga 49

<210> 111  
 <211> 31  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> primer  
  
 <400> 111  
 atcctcgaga gagattctgc ggaggagctt c 31  
  
 <210> 112  
 <211> 34  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> primer  
  
 <400> 112  
 atcggatcca tggttctgca gaaaaccaaa agca 34  
  
 <210> 113  
 <211> 32  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> primer  
  
 <400> 113  
 atctctagat gaggatgatg gtgaagaaat tg 32  
  
 <210> 114  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> primer  
  
 <400> 114  
 atcaagctta ctgtccgaag gtcacatttc 30  
  
 <210> 115  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> primer  
  
 <400> 115  
 ggaatgcatg tacatcgagc c 21  
  
 <210> 116  
 <211> 21

<212> DNA  
 <213> Artificial Sequence

<220>  
 <223> primer

<400> 116  
 ggaacttggtg ttggcatggt g 21

<210> 117  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> primer

<221> misc\_feature  
 <222> 6, 9  
 <223> n = A,T,C or G

<400> 117  
 tggccngtnt aytggttytg 20

<210> 118  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> primer

<221> misc\_feature  
 <222> 6  
 <223> n = A,T,C or G

<400> 118  
 tcyttngcyt cyctccacat 20

<210> 119  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> primer

<400> 119  
 atgggtgctg gtggtcggat g 21

<210> 120  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> primer

<400> 120  
 gaacacgctt acacctagga c 21

<210> 121  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> primer

<400> 121  
 atcaatccac tggattcac 20

<210> 122  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> primer

<400> 122  
 gtcctaggtg taagcgtg 18

<210> 123  
 <211> 29  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> primer

<400> 123  
 aagcttacca tgggtgccca cggccatgg 29

<210> 124  
 <211> 31  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> primer

<400> 124  
 ggcgcgccac catgggtgcc cacggccatg g 31

<210> 125  
 <211> 383  
 <212> PRT  
 <213> Arabidopsis thaliana

<400> 125  
 Met Gly Ala Gly Gly Arg Met Pro Val Pro Thr Ser Ser Lys Lys Ser  
 1 5 10 15  
 Glu Thr Asp Thr Thr Lys Arg Val Pro Cys Glu Lys Pro Pro Phe Ser

			20					25				30			
Val	Gly	Asp	Leu	Lys	Lys	Ala	Ile	Pro	Pro	His	Cys	Phe	Lys	Arg	Ser
		35					40					45			
Ile	Pro	Arg	Ser	Phe	Ser	Tyr	Leu	Ile	Ser	Asp	Ile	Ile	Ile	Ala	Ser
		50				55					60				
Cys	Phe	Tyr	Tyr	Val	Ala	Thr	Asn	Tyr	Phe	Ser	Leu	Leu	Pro	Gln	Pro
65					70					75					80
Leu	Ser	Tyr	Leu	Ala	Trp	Pro	Leu	Tyr	Trp	Ala	Cys	Gln	Gly	Cys	Val
				85					90					95	
Leu	Thr	Gly	Ile	Trp	Val	Ile	Ala	His	Glu	Cys	Gly	His	His	Ala	Phe
			100					105					110		
Ser	Asp	Tyr	Gln	Trp	Leu	Asp	Asp	Thr	Val	Gly	Leu	Ile	Phe	His	Ser
		115					120					125			
Phe	Leu	Leu	Val	Pro	Tyr	Phe	Ser	Trp	Lys	Tyr	Ser	His	Arg	Arg	His
		130				135						140			
His	Ser	Asn	Thr	Gly	Ser	Leu	Glu	Arg	Asp	Glu	Val	Phe	Val	Pro	Lys
145					150					155					160
Gln	Lys	Ser	Ala	Ile	Lys	Trp	Tyr	Gly	Lys	Tyr	Leu	Asn	Asn	Pro	Leu
				165				170						175	
Gly	Arg	Ile	Met	Met	Leu	Thr	Val	Gln	Phe	Val	Leu	Gly	Trp	Pro	Leu
			180					185					190		
Tyr	Leu	Ala	Phe	Asn	Val	Ser	Gly	Arg	Pro	Tyr	Asp	Gly	Phe	Ala	Cys
		195					200					205			
His	Phe	Phe	Pro	Asn	Ala	Pro	Ile	Tyr	Asn	Asp	Arg	Glu	Arg	Leu	Gln
		210				215					220				
Ile	Tyr	Leu	Ser	Asp	Ala	Gly	Ile	Leu	Ala	Val	Cys	Phe	Gly	Leu	Tyr
225					230					235					240
Arg	Tyr	Ala	Ala	Ala	Gln	Gly	Met	Ala	Ser	Met	Ile	Cys	Leu	Tyr	Gly
				245					250					255	
Val	Pro	Leu	Leu	Ile	Val	Asn	Ala	Phe	Leu	Val	Leu	Ile	Thr	Tyr	Leu
			260					265						270	
Gln	His	Thr	His	Pro	Ser	Leu	Pro	His	Tyr	Asp	Ser	Ser	Glu	Trp	Asp
		275					280						285		
Trp	Leu	Arg	Gly	Ala	Leu	Ala	Thr	Val	Asp	Arg	Asp	Tyr	Gly	Ile	Leu
		290				295					300				
Asn	Lys	Val	Phe	His	Asn	Ile	Thr	Asp	Thr	His	Val	Ala	His	His	Leu
305					310					315					320
Phe	Ser	Thr	Met	Pro	His	Tyr	Asn	Ala	Met	Glu	Ala	Thr	Lys	Ala	Ile
			325						330					335	
Lys	Pro	Ile	Leu	Gly	Asp	Tyr	Tyr	Gln	Phe	Asp	Gly	Thr	Pro	Trp	Tyr
			340					345					350		
Val	Ala	Met	Tyr	Arg	Glu	Ala	Lys	Glu	Cys	Ile	Tyr	Val	Glu	Pro	Asp
		355					360					365			
Arg	Glu	Gly	Asp	Lys	Lys	Gly	Val	Tyr	Trp	Tyr	Asn	Asn	Lys	Leu	
		370				375						380			

&lt;210&gt; 126

&lt;211&gt; 384

&lt;212&gt; PRT

&lt;213&gt; Brassica napus

&lt;400&gt; 126

Met	Gly	Ala	Gly	Gly	Arg	Met	Gln	Val	Ser	Pro	Pro	Ser	Lys	Lys	Ser
1				5					10					15	
Glu	Thr	Asp	Thr	Ile	Lys	Arg	Val	Pro	Cys	Glu	Thr	Pro	Pro	Phe	Thr
			20					25					30		
Val	Gly	Glu	Leu	Lys	Lys	Ala	Ile	Pro	Pro	His	Cys	Phe	Lys	Arg	Ser

	35					40					45				
Ile	Pro	Arg	Ser	Phe	Ser	Tyr	Leu	Ile	Trp	Asp	Ile	Ile	Ile	Ala	Ser
	50					55					60				
Cys	Phe	Tyr	Tyr	Val	Ala	Thr	Thr	Tyr	Phe	Pro	Leu	Leu	Pro	His	Pro
65					70					75					80
Leu	Ser	Tyr	Phe	Ala	Trp	Pro	Leu	Tyr	Trp	Ala	Cys	Gln	Gly	Cys	Val
				85					90					95	
Leu	Thr	Gly	Val	Trp	Val	Ile	Ala	His	Glu	Cys	Gly	His	His	Ala	Phe
			100					105					110		
Ser	Asp	Tyr	Gln	Trp	Leu	Asp	Asp	Thr	Val	Gly	Leu	Ile	Phe	His	Ser
		115				120						125			
Phe	Leu	Val	Pro	Tyr	Phe	Ser	Trp	Lys	Tyr	Ser	His	Arg	Arg	His	
	130				135					140					
His	Ser	Asn	Thr	Gly	Ser	Leu	Glu	Arg	Asp	Glu	Val	Phe	Val	Pro	Lys
145					150					155					160
Lys	Lys	Ser	Asp	Ile	Lys	Trp	Tyr	Gly	Lys	Tyr	Leu	Asn	Asn	Pro	Leu
				165					170					175	
Gly	Arg	Thr	Val	Met	Leu	Thr	Val	Gln	Phe	Thr	Leu	Gly	Trp	Pro	Leu
			180					185					190		
Tyr	Leu	Ala	Phe	Asn	Val	Ser	Gly	Arg	Pro	Tyr	Asp	Gly	Gly	Phe	Ala
	195					200						205			
Cys	His	Phe	His	Pro	Asn	Ala	Pro	Ile	Tyr	Asn	Asp	Arg	Glu	Arg	Leu
	210					215					220				
Gln	Ile	Tyr	Ile	Ser	Asp	Ala	Gly	Ile	Leu	Ala	Val	Cys	Tyr	Gly	Leu
225					230					235					240
Phe	Arg	Tyr	Ala	Ala	Ala	Gln	Gly	Val	Ala	Ser	Met	Val	Cys	Phe	Tyr
			245						250					255	
Gly	Val	Pro	Leu	Leu	Ile	Val	Asn	Gly	Leu	Leu	Val	Leu	Ile	Thr	Tyr
			260					265					270		
Leu	Gln	His	Thr	His	Pro	Ser	Leu	Pro	His	Tyr	Asp	Ser	Ser	Glu	Trp
	275					280						285			
Asp	Trp	Leu	Arg	Gly	Ala	Leu	Ala	Thr	Val	Asp	Arg	Asp	Tyr	Gly	Ile
	290					295					300				
Leu	Asn	Lys	Val	Phe	His	Asn	Ile	Thr	Asp	Thr	His	Val	Ala	His	His
305					310					315					320
Leu	Phe	Ser	Thr	Met	Pro	His	Tyr	His	Ala	Met	Glu	Ala	Thr	Lys	Ala
				325					330					335	
Ile	Lys	Pro	Ile	Leu	Gly	Glu	Tyr	Tyr	Gln	Phe	Asp	Gly	Thr	Pro	Val
			340					345					350		
Val	Lys	Ala	Met	Trp	Arg	Glu	Ala	Lys	Glu	Cys	Ile	Tyr	Val	Glu	Pro
	355						360					365			
Asp	Arg	Gln	Gly	Glu	Lys	Lys	Gly	Val	Phe	Trp	Tyr	Asn	Asn	Lys	Leu
	370					375						380			

<210> 127

<211> 383

<212> PRT

<213> Glycine max

<400> 127

Met	Gly	Ala	Gly	Gly	Arg	Thr	Asp	Val	Pro	Pro	Ala	Asn	Arg	Lys	Ser
1				5					10					15	
Glu	Val	Asp	Pro	Leu	Lys	Arg	Val	Pro	Phe	Glu	Lys	Pro	Gln	Phe	Ser
			20					25					30		
Leu	Ser	Gln	Ile	Lys	Lys	Ala	Ile	Pro	Pro	His	Cys	Phe	Gln	Arg	Ser
		35				40					45				
Val	Leu	Arg	Ser	Phe	Ser	Tyr	Val	Val	Tyr	Asp	Leu	Thr	Ile	Ala	Phe

50						55					60				
Cys	Leu	Tyr	Tyr	Val	Ala	Thr	His	Tyr	Phe	His	Leu	Leu	Pro	Gly	Pro
65					70					75					80
Leu	Ser	Phe	Arg	Gly	Met	Ala	Ile	Tyr	Trp	Ala	Val	Gln	Gly	Cys	Ile
				85					90					95	
Leu	Thr	Gly	Val	Trp	Val	Ile	Ala	His	Glu	Cys	Gly	His	His	Ala	Phe
			100					105						110	
Ser	Asp	Tyr	Gln	Leu	Leu	Asp	Asp	Ile	Val	Gly	Leu	Ile	Leu	His	Ser
		115					120							125	
Ala	Leu	Leu	Val	Pro	Tyr	Phe	Ser	Trp	Lys	Tyr	Ser	His	Arg	Arg	His
						135								140	
His	Ser	Asn	Thr	Gly	Ser	Leu	Glu	Arg	Asp	Glu	Val	Phe	Val	Pro	Lys
145						150				155					160
Gln	Lys	Ser	Cys	Ile	Lys	Trp	Tyr	Ser	Lys	Tyr	Leu	Asn	Asn	Pro	Pro
				165						170					175
Gly	Arg	Val	Leu	Thr	Leu	Ala	Val	Thr	Leu	Thr	Leu	Gly	Trp	Pro	Leu
			180					185						190	
Tyr	Leu	Ala	Leu	Asn	Val	Ser	Gly	Arg	Pro	Tyr	Asp	Arg	Phe	Ala	Cys
		195					200						205		
His	Tyr	Asp	Pro	Tyr	Gly	Pro	Ile	Tyr	Ser	Asp	Arg	Glu	Arg	Leu	Gln
		210				215								220	
Ile	Tyr	Ile	Ser	Asp	Ala	Gly	Val	Leu	Ala	Val	Val	Tyr	Gly	Leu	Phe
225					230					235					240
Arg	Leu	Ala	Met	Ala	Lys	Gly	Leu	Ala	Trp	Val	Val	Cys	Val	Tyr	Gly
				245					250						255
Val	Pro	Leu	Leu	Val	Val	Asn	Gly	Phe	Leu	Val	Leu	Ile	Thr	Phe	Leu
			260					265						270	
Gln	His	Thr	His	Pro	Ala	Leu	Pro	His	Tyr	Thr	Ser	Ser	Glu	Trp	Asp
		275						280						285	
Trp	Leu	Arg	Gly	Ala	Leu	Ala	Thr	Val	Asp	Arg	Asp	Tyr	Gly	Ile	Leu
		290				295						300			
Asn	Lys	Val	Phe	His	Asn	Ile	Thr	Asp	Thr	His	Val	Ala	His	His	Leu
305					310					315					320
Phe	Ser	Thr	Met	Pro	His	Tyr	His	Ala	Met	Glu	Ala	Thr	Lys	Ala	Ile
				325					330						335
Lys	Pro	Ile	Leu	Gly	Glu	Tyr	Tyr	Arg	Phe	Asp	Glu	Thr	Pro	Phe	Val
			340					345						350	
Lys	Ala	Met	Trp	Arg	Glu	Ala	Arg	Glu	Cys	Ile	Tyr	Val	Glu	Pro	Asp
		355					360							365	
Gln	Ser	Thr	Glu	Ser	Lys	Gly	Val	Phe	Trp	Tyr	Asn	Asn	Lys	Leu	
	370					375								380	

&lt;210&gt; 128

&lt;211&gt; 383

&lt;212&gt; PRT

&lt;213&gt; Sesamum indicum

&lt;400&gt; 128

Met	Gly	Ala	Gly	Gly	Arg	Met	Ser	Asp	Pro	Thr	Thr	Lys	Asp	Glu	Gln
1				5					10					15	
Lys	Lys	Asn	Pro	Leu	Gln	Arg	Val	Pro	Tyr	Ala	Lys	Pro	Pro	Phe	Thr
			20					25						30	
Leu	Gly	Asp	Ile	Lys	Lys	Ala	Ile	Pro	Pro	His	Cys	Phe	Glu	Arg	Ser
		35					40					45			
Val	Ser	Arg	Ser	Phe	Ser	Tyr	Val	Val	Tyr	Asp	Leu	Val	Ile	Val	Phe
	50					55					60				
Leu	Leu	Tyr	Tyr	Ile	Ala	Thr	Ser	Tyr	Phe	His	Leu	Leu	Pro	Ser	Pro



65					70					75					80
Tyr	Cys	Tyr	Leu	Ala	Trp	Pro	Ile	Tyr	Trp	Ala	Val	Gln	Gly	Cys	Val
				85					90					95	
Cys	Thr	Gly	Ile	Trp	Val	Ile	Ala	His	Glu	Cys	Gly	His	His	Ala	Phe
			100					105						110	
Ser	Asp	Tyr	Gln	Trp	Leu	Asp	Asp	Thr	Val	Gly	Leu	Ile	Leu	His	Ser
		115					120							125	
Ala	Leu	Leu	Val	Pro	Tyr	Phe	Ser	Trp	Lys	Tyr	Ser	His	Arg	Arg	His
	130					135					140				
His	Ser	Asn	Thr	Gly	Ser	Leu	Glu	Arg	Asp	Glu	Val	Phe	Val	Pro	Lys
145					150					155					160
Pro	Lys	Ser	Arg	Val	Ser	Trp	Tyr	Ser	Lys	Tyr	Leu	Asn	Asn	Pro	Leu
				165					170					175	
Gly	Arg	Val	Ile	Thr	Leu	Val	Val	Thr	Leu	Thr	Leu	Gly	Trp	Pro	Leu
			180					185						190	
Tyr	Leu	Leu	Phe	Asn	Val	Ser	Gly	Arg	Pro	Tyr	Asn	Arg	Phe	Ala	Cys
	195						200					205			
His	Phe	Asp	Pro	Tyr	Gly	Pro	Ile	Tyr	Asn	Asp	Arg	Glu	Arg	Leu	Gln
	210					215					220				
Ile	Phe	Ile	Ser	Asp	Ala	Gly	Ile	Ile	Ala	Ala	Val	Cys	Val	Leu	Tyr
225					230					235					240
Arg	Val	Ala	Leu	Val	Lys	Gly	Leu	Ala	Trp	Leu	Val	Cys	Val	Tyr	Gly
				245					250					255	
Val	Pro	Leu	Leu	Ile	Val	Asn	Gly	Phe	Leu	Val	Leu	Ile	Thr	Phe	Leu
			260					265						270	
Gln	His	Thr	His	Pro	Ser	Leu	Pro	His	Tyr	Asp	Ser	Ser	Glu	Trp	Asp
		275					280					285			
Trp	Leu	Arg	Gly	Ala	Leu	Ala	Thr	Val	Asp	Arg	Asp	Tyr	Gly	Val	Leu
	290					295					300				
Asn	Lys	Val	Phe	His	Asn	Ile	Thr	Asp	Thr	His	Val	Thr	His	His	Leu
305					310					315					320
Phe	Ser	Thr	Met	Pro	His	Tyr	His	Ala	Met	Glu	Ala	Thr	Lys	Ala	Ile
			325						330					335	
Lys	Pro	Ile	Leu	Gly	Gln	Tyr	Tyr	Gln	Phe	Asp	Gly	Thr	Pro	Phe	Tyr
			340					345					350		
Lys	Ala	Met	Trp	Arg	Glu	Ala	Lys	Glu	Cys	Leu	Tyr	Val	Glu	Pro	Asp
	355						360					365			
Glu	Ser	Thr	Pro	Asp	Lys	Gly	Val	Phe	Trp	Tyr	Lys	Asn	Lys	Phe	
	370					375					380				

<210> 129

<211> 9

<212> PRT

<213> Human influenza virus

<400> 129

Tyr Pro Tyr Asp Val Pro Asp Tyr Ala

1

5

<210> 130

<211> 12

<212> DNA

<213> Ricinus communis

<400> 130

agaaaggagg aa